

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:37:39 ; Search time 78.6609 Seconds
(without alignments)
1323.818 Million cell updates/sec

Title: US-10-828-782A-16

Perfect score: 1332
Sequence: 1 MKLPLRLVLMFMI PASSSD.....EVTHQGLSPVTKFNRGEC 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1232	100.0	237	9	ADU70077 Mouse/hum
2	1175.5	95.4	238	2	AAW14937 Murine an
3	1175.5	95.4	238	2	AAW14942 3F4 Human
4	1164.5	94.5	238	6	ABP58288 Humanised
5	1113.5	90.4	238	6	AAU07744 Humanised
6	1113.5	90.4	238	6	ABR39842 Humanised
7	1106	89.8	238	6	ADS88785 Sequence
8	1103.5	88.6	219	8	ADP84971 Chimeric
9	1094	88.8	239	2	AAW71876 Anti-huma
10	1094	88.8	239	2	AAW12913 Anti-huma
11	1091	88.6	239	2	AAW71878 Anti-huma
12	1091	88.6	239	2	AAW12915 Anti-huma
13	1090	88.5	239	2	AAW71877 Anti-huma
14	1090	88.5	239	2	AAW12914 Anti-huma
15	1089.5	88.4	219	9	ADW77072 Light Cha
16	1087	88.2	239	2	AAW71879 Anti-huma
17	1087	88.2	239	2	AAW12916 Anti-huma
18	1086.5	88.2	219	8	ADP19331 Chimeric
19	1068.5	86.8	219	8	ABP58286 Humanised
20	1049	85.1	239	9	ABE45871 Human mon
21	1046	84.9	239	9	ABE45903 Human mon
22	1043	84.7	239	9	AAW82615 Human PTH
23	1043	84.7	239	9	ABE45879 Human mon
24	1043	84.7	242	2	AAW86323 Chimeric

25	1043	84.7	242	2	AAW23790 Chimeric
26	1043	84.7	242	2	AAW31580 Chimeric
27	1043	84.7	242	2	AAW42323 Murine va
28	1043	84.7	242	2	AAW33745 Chimeric
29	1043	84.7	242	2	AAW69311 Anti-IL-8
30	1043	84.7	242	2	AAW40126 Chimeric
31	1043	84.7	242	2	AAW29442 Chimeric
32	1043	84.7	242	3	AAW77748 Chimeric
33	1043	84.7	242	3	AAW30305 Murine 6G
34	1043	84.7	242	6	ABU13782 Mouse ant
35	1043	84.7	242	6	ABU59495 Mouse ant
36	1043	84.7	242	7	AAE39078 Murine 6G
37	1039	84.3	239	7	AAE28421 Human ant
38	1036	84.1	239	3	AAW82617 Human PTH
39	1032	83.8	239	7	ADP28461 Human ant
40	1030	83.6	220	8	ADP42960 Humanised
41	1030	83.6	220	9	ABE43844 Human HUI
42	1030	83.6	239	3	AAW82611 Human PTH
43	1030	83.6	239	7	ADP28465 Human ant
44	1029	83.5	239	2	AAW01819 Primatice
45	1029	83.5	239	2	AAW63762 Macaque p

ALIGNMENTS

RESULT 1	ADU70077	ADU70077 standard; protein; 237 AA.
XX	ADU70077;	
AC	ADU70077;	
XX	24-FEB-2005 (first entry)	
DT		
XX	Mouse/human chimeric monoclonal antibody 6B5 light chain, SEQ:16.	
DE	Antibody engineering; chimeric antibody; drug dependence; phenylalidine;	
XX	PCP; antidiabetic; toxicity; toxicity; intoxication;	
KW	psychiatric disorder; immunoglobulin; chimeric monoclonal antibody 6B5;	
KM	ch-mab6B5; light chain.	
XX		
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX	US2004242848-A1.	
XX		
PD	02-DEC-2004.	
XX		
PP	21-APR-2004; 2004US-00828782.	
XX		
FR	21-APR-2003; 2003US-0464190P.	
XX		
PA	(OWEN/) OWENS S M.	
XX	(LACY/) LACY H M.	
XX		
PI	Owens SM, Lacy HM;	
XX		
DR	WPI; 2005-011672/01.	
DR	N-PSDB; ADU70076.	
XX		
PT	New chimeric mouse/human monoclonal antibody for treating phenylalidine	
PT	drug abuse and toxicity comprises human immunoglobulin constant domains	
PT	and immunoglobulin variable domains of murine antibody.	
XX		
PS	Claim 4; SEQ ID NO 16; 34pp; English.	
XX		
CC	The invention relates to a chimeric mouse/human monoclonal antibody named	
CC	ch-mab6B5 (see ADU70077 and ADU70079) which is specific for phenylalidine	
CC	(PCP). ch-mab6B5 comprises immunoglobulin constant domains of human	
CC	origin and immunoglobulin variable domains from the murine anti-PCP	
CC	monoclonal antibody 6B5. The invention also relates to DNA sequences	
CC	encoding the light and heavy chains of the chimeric antibody (ADU70076	

CC host cells comprising either of these DNA sequences; the recombinant
CC and ADU70078 respectively); to expression vectors and mammalian or plant
CC production of the chimeric antibody; a pharmaceutical composition
CC comprising the chimeric antibody; and a method of treating
CC arylcyclohexylamine drug abuse using the chimeric antibody. The chimeric
CC antibody reverses and/or reduces the adverse effects of
CC arylcyclohexylamine drug abuse. The chimeric antibody, compositions
CC comprising it and method of the invention are useful for treating abuse
CC and toxicity of the arylcyclohexylamine class of drugs such as PCP, 1-(1-
CC (2-phenyl) cyclohexyl) piperidine (TCP) and N-ethyl-1-
CC phenylcyclohexylamine (PCP) or other structurally similar, psychoactive
CC analogs. The present sequence represents the chimeric light chain of ch-
CC mAb6B5.

SQ Sequence 237 AA;

Query Match	100.0%	Score 1232;	DB 9	Length 237;
Best Local Similarity	100.0%	Pred. No. 3.2e-69;		
Matches 237; Conservative	0;	Mismatches	0;	Indels 0
				Gaps 0

Qy	1	MKLPVLLVLMFVIIPASSSDVLMTCQPLSLPVSLDQASISCRSSQITVHNSGNTVLEMY	60
Db	1	MKLPVLLVLMFVIIPASSSDVLMTCQPLSLPVSLDQASISCRSSQITVHNSGNTVLEMY	60
Qy	61	LQKPGQSPKLLIYKVSNNRPSGVAPDRPSGSGSTDTLKIISRAVEDIGVYCYFGQTHAPY	120
Db	61	LQKPGQSPKLLIYKVSNNRPSGVAPDRPSGSGSGTDTLKIISRAVEDIGVYCYFGQTHAPY	120
Qy	121	TBGGGTRKLEKTKAAASVFIIPPSDQLKSGTASVYCLNNFYPREANVQKMDNALQSG	180
Db	121	TBGGGTRKLEKTKAAASVFIIPPSDQLKSGTASVYCLNNFYPREANVQKMDNALQSG	180
Qy	181	NSQESVTEEDSKOSTVSLSTLTLSKADYEKKHVACVETHQGLSSPTVSKFNNRGEC	237
Db	181	NSQESVTEEDSKOSTVSLSTLTLSKADYEKKHVACVETHQGLSSPTVSKFNNRGEC	237

RESULT 2
AAW14937

XX
AC AAW14937;

DT 16-JUN-1997 (first entry)
xx

DE Murine anti-porcine VCAM 3F4 light chain

KM Xenotransplantation; graft rejection; cell interaction; pig;
KM vascular cell adhesion molecule; VCAM; monoclonal antibody;
KM chimeric antibody; diagnosis.

OS Mus sp.

FH	Key	Location/Qualifiers

FT	Position
FT	/Label= CDR1
FT	74 80

FT	Region
113	121

XX: 1432341 0200

PN WO9711971-A1

PD 03-APR-1997

PF 27-SEP-1996; 96WO-US015575

PR 28-SEP-1995; 95US-0004489P
PR 26-SEP-1996; 96US-00004489

PA (ALEX-) ALEXION PHARM INC

PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA,

XX	
DR	WPI; 1997-212855/19.
DR	N-PSDB; AAT62934.
XX	

PT Antibodies binding to porcine but not human cell interaction proteins
PT useful to treat and assay for rejection of xenografted porcine organs,
PT tissues or cells.

PS Disclosure; Page 52-53; 105pp; English.

CC Light chain (AAW14937) and heavy chain (AAW14938) sequences are provided
CC for the murine anti-porcine soluble vascular cell adhesion molecule
CC (VCAM) monoclonal antibody (Mab) 3F4. Hybridoma 3F4 was produced by
CC standard techniques using recombinant, soluble porcine VCAM as immunogen.
CC Chimeric antibodies can be produced by cloning Mab 3F4 and 2A2 (see also
CC AAW14931-32) variable regions into expression plasmid pADEX-3P modified
CC to contain the human gamma4 constant region in place of the human gamma1
CC C1 region. Sequences are provided for 3F4 (chimeric) human G2/G4 cDNA
CC (AAW14930), a 3F4 human G2/G4 expression plasmid insert product
CC (AAW14940), and 3F4 human IgG4 expression plasmid insert products
CC (AAW14941-42). The chimeric antibodies are specific for porcine VCAM.
CC They are useful for diagnosing human rejection of porcine xenotransplants
CC and for improving xenotransplantation of porcine cells, tissues and
CC organs into human recipients

SQ Sequence 238 AA;

Query Match	95.4%	Score 1175.5	DB 2	Length 238
Best Local Similarity	95.0%	Pred. No. 1.1e-65		
Matches 226	Conservative	6	Mismatches 5	Indels 1
			Gaps	1

Qy	1	MKLPVLLVLMFPIPASSSDVLMQTPTSLPVLSDQASISCRSSQITVHNGNTYILEMY	60
		1	1
Db	1	MKLPVLLVLMFPIPASSSDVLMQTPTSLPVLSDQASISCRSSQISVHNGNTYILQMY	60
Qy	61	LQRPQGSFKLLIKVYSNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGTAPY	120
		61	1
Db	61	LQRPQGSFKLLIKVYSNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGTAPV	120
Qy	121	TFGGQTKLIRK-TAAAPSVFIIPPSPDQQLKSTASVGLINFPYPRKAKQMKVDNALQS	175
		121	1
Db	121	TFGGQTKLIRKRVAAAPSVFIIPPSPDQQLKSTASVGLINFPYPRKAKQMKVDNALQS	180
Qy	180	GNQGSVTEBDQSDQSYSLSTLLTSKADYRHKYACELTHQGLSPVYTKSPFRGEC	237
		181	1
Db	181	GNQGSVTEBDQSDQSYSLSTLLTSKADYRHKYACAEVTHQGLSPVYTKSPFRGEC	238

RESULT 3

AAWL4942
ID AAWL4942 standard; protein; 238 AA.

AC AAW14942;

DT 16-JUN-1997 (first entry)

DE 3F4 Human IgG4 expression plasmid insert product (light chain)

KM vascular cell adhesion molecule; VCAM; monoclonal antibody;
KM chimeric antibody; diagnosis.

OS Mus sp.

PN MO9711971-A1.

PD 03-APR-15
YY

PF 27-SEP-1996; 96WO-US015575.
XX

PR	26-SEP-1995;	95US-0004489P.
PR	26-SEP-1996;	96US-00004489.
XX		

XX

PA	(ALEX-)	ALEXION PHARM INC.
XX		
PI	Mueller JP,	Evans MJ, Mueller EE, Rollins S, Rother RP, Matlis LA;
DR	WP1; 1997-212855/19.	
DR	N-PsDBJ; AAT62938.	
XX		
PT	Antibodies binding to porcine but not human cell interaction proteins -	
PT	useful to treat and assay for rejection of xenografted porcine organs,	
FT	tissues or cells.	
PS	Disclosure; Page 65-66; 105pp; English.	
XX		
CC	Heavy chain (AAW14941) and light chain (AAW14942) sequences correspond to	
CC	murine anti-porcine soluble vascular cell adhesion molecule (VCAM)	
CC	monoclonal antibody 3F4 (see also AAW14937-38). They are encoded by a 3F4	
CC	human IgG4 expression plasmid insert (see also AAT62938). A chimeric	
CC	antibody specific for porcine VCAM can be produced in transfected host	
CC	cells. It is useful for diagnosing human rejection of porcine	
CC	xenotransplants and for improving xenotransplantation of porcine cells,	
CC	tissues and organs into human recipients	
SQ	Sequence 238 AA;	
Query Match	95.4%; Score 1175.5; DB 2; Length 238;	
Best Local Similarity	95.0%; Pred. No. 1.le-65;	
Matches 226; Conservative 6; Mismatches 5; Indels 1; Gaps 1;		
OY	1 MKLPRLILVLMFWIPASSDVLMTOTPLSLPVSIGDOASISGRSSQTIHNSGNTLYEMV 60	
Dd	1 MKLPRLILVLMFWIPVSSDDVMVTPLSPVLSLDDOASISGRSSQSIHNSGNTLYOMV 60	
OY	61 LQKRGQSFKLIYYKVSNNRFSGVPRFSGSGSGSTDTFLKISRVEADLVGYCYFCGTNAPY 120	
Dd	61 LQKRGQSFKLIYYKVSNNRFSGVPRFSGSGSGSTDTFLKISRVEADLVGYCYFCGTNAPY 120	
OY	121 TFGGGTCLKLR-TAAPSVFIFPPSDEQLKSGTASVCLINNFPREAKVQMKVDNALQS 179	
Dd	121 TFGGGTCLKLRITRYAAPSVFIFFPPSDEQLKSGTASVCLINNFPREAKVQMKVDNALQS 180	
OY	180 GNSQESVTEODSKOSTYSLSLTLSKDYERHKHYACEVTHQGISSPVTSFNNGEC 237	
Dd	181 GNSQESVTEODSKOSTYSLSLTLSKDYERHKHYACEVTHQGISSPVTSFNNGEC 238	
RESULT 4		
ABP58288	ABP58288 standard; protein; 238 AA.	
XX		
AC	ABP58288;	
XX		
DT	23-OCT-2003 (revised)	
DT	31-MAR-2003 (first entry)	
DE	Humanised 10D5 antibody light chain.	
XX		
KW	Monoclonal antibody; 10D5; complementarity determining region; CDR;	
KM	mouse; human; humanised antibody; antibody; Alzheimer's disease;	
XX	Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.	
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
FH	.Key	
FT	Peptide	Location/Qualifiers
FT	Peptide	1..19
FT	Peptide	/label= Signal_peptide
FT	Peptide	20..238
FT	Region	/label= Mature_protein
FT	Region	/note= "the mature light chain is claimed in Claim 5"
FT	Region	20..132
FT	Region	/note= "light chain variable region, claimed in Claim 4"
FT	Region	43..58

FT	/note= "CDR1"
FT	74..80
FT	/note= "CDR2"
FT	113..121
FT	Region .
FT	/note= "CDR3"
PX	
XX	WO20028307-A2.
XX	
PD	07-NOV-2002.
XX	
PF	26-APR-2002; 2002WO-US011854.
XX	
PR	30-APR-2001; 2001US-0287653P.
PA	(LILLY & CO ELI.
PI	Hinton PR, Vasquez M;
XX	
DR	WPI; 2003-183836/18
XX	N-PSDB; ABZ24638, ABZ24640.
PT	New humanized 10D5 antibody, useful for the manufacture of a medicament
PT	for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT	disease or cerebral amyloid angiopathy.
XX	
PS	Disclosure; Page 13; 52pp; English.
CC	The present sequence is the protein sequence of the light chain of a
CC	humanised antibody of the present invention. In the variable portion, the
CC	complementarity determining regions (CDRs) originate from murine
CC	monoclonal antibody 10D5 and the framework region originates from human
CC	germline VK segment DPK18 and J segment JK4. Novel humanised antibodies
CC	of the invention have CDRs from 10D5 and human framework sequences. These
CC	humanised antibodies have binding affinities (affinity and epitope
CC	location) approximately the same as those of the mouse 10D5 antibody. The
CC	invention includes antibodies, single chain antibodies, and their
CC	fragments, as well as nucleotide sequences, vectors, transformed host
CC	cells, and methods of using the humanised antibody to treat, prevent,
CC	alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC	associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC	(pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC	reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC	OS field)
SQ	Sequence 238 AA;
Query Match	94.5%; Score 1164.5; DB 6; Length 238;
Best Local Similarity	93.7%; Pred. No.5.2e-65;
Matches 223; Conservative	8; Mismatches 6; Indels 1; Gaps 1
Dd	
QY	1 MKLPRLVLVLFMWIPASSSDVLTMTQTPLSLSPVLSIGDDQSISCRSSQTIIVHNGNTYLEMY 60
	::: ::: ::: ::: ::: ::: ::: :::
Dd	1 MKLPRLVLVLFMWIPASSSDVVTQSPSLSVTLTGQPASISCRSQNIHNSGNTILEMY 60
	::: ::: ::: ::: ::: ::: :::
Dd	61 LQKQGQSPRLLIYKVSNRNFSGVPPRFSGSGSGETFTLKISRVEADLVGYTCFQGTAAFY 120
	::: ::: ::: ::: ::: ::: :::
QY	61 LQKQGQSPRLLIYKVSNRNFSGVPPRFSGSGSGETFTLKISRVEADLVGYTCFQGTAAFY 120
	::: ::: ::: ::: ::: ::: :::
Dd	61 LQKQGQSPRLLIYKVSNRNFSGVPPRFSGSGSGETFTLKISRVEADLVGYTCFQGSHPVL 120
	::: ::: ::: ::: ::: ::: :::
QY	121 TFGGGTKLEIK-TAASPVFIFPPSDDELKSGTASVCLLNFFPREAKVQMKNDAALQS 179
	::: ::: ::: ::: ::: ::: :::
Dd	121 TFGGGITKEIKRTVAAPSVFIAPPSEDLKSGTASVCLLNFFPREAKVQMKNDAALQS 180
	::: ::: ::: ::: ::: ::: :::
QY	180 GNSGESVTEODSKDSTYSLSSTLTLSKADYEKKHKVYACEVTHOGLSSEPVTSFNRGEC 237
	::: ::: ::: ::: ::: ::: :::
Dd	181 GNSGESVTEODSKDSTYSLSSTLTLSKADYEKKHKVYACEVTHOGLSSSEPVTSFNRGEC 238
	::: ::: ::: ::: ::: ::: :::
RESULT 5	
ID	AAU07744
AC	AAU07744 standard; protein; 238 AA.
XX	AAU07744;
XX	

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DT 04-DEC-2001 (first entry)
XX Humanised monoclonal antibody Hu266, light chain.
XX
XX Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
XX Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
XX gene therapy.
XX
XX Mus sp.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= Signal_peptide
XX Protein 20..238
XX /label= Mature_Hu266_light_chain
XX /note= "This sequence is specifically claimed in claim
XX 17"
XX
XX WO200162801-A2.
XX
XX 30-AUG-2001.
XX
XX 26-FEB-2001; 2001WO-US006191.
XX
XX 24-FEB-2000; 2000US-0184601P.
XX 08-DEC-2000; 2000US-0254465P.
XX 08-DEC-2000; 2000US-0254498P.
XX
XX (UNIT ) UNIV WASHINGTON.
XX (ELIL ) LILLY & CO ELL.
XX
XX Holtzman DM, Dematos R, Bales KR, Paul SM, Teuruehita N;
XX Vaquez M;
XX
XX WPI: 2001-550087/61.
XX N-PSDB; AAS11981.
XX
XX New humanised antibody for the treatment of Alzheimer's comprises the
XX inhibition and reduction of the formation of amyloid plaques.
XX
XX Example 13; Fig 4; 63pp; English.
XX
XX The invention relates a humanised antibody that specifically binds an
XX epitope contained within positions 13-28 of amyloid beta peptide, Abeta.
XX The antibody is useful to inhibit and reduce the formation of amyloid
XX plaques or the effects of toxic soluble Abeta species in humans their
XX fragments are used for the manufacture of a medicant. This includes the
XX prolonged expression of recombinant sequences of them in human tissues
XX for the treatment of clinical/pre-clinical Alzheimer's disease, Down's
XX syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the
XX antibody is used to sequester Abeta into plasma, brain or cerebrospinal
XX fluid to prevent/reverse accumulation of the Abeta peptide within the
XX brain thereby improving cognition. The present sequence is the light
XX chain of a humanised monoclonal antibody, Hu266, based on the mouse
XX antibody 266
XX
XX Sequence 238 AA;
XX
XX Query Match 90.4%; Score 1113.5; DB 4; Length 238;
XX Best Local Similarity 89.5%; Pred. No. 7.9e-62;
XX Matches 213; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
XX
XX 1 MCLPRLVLMFWIPASSSDVMTOTPLSLPVSIGDQASISCRSSQTIYHSNGNTLYEMV 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 MCLPRLVLMFWIPASSSDVMTOTPLSLPVSIGDQASISCRSSQTIYHSNGNTLYEMV 60
XX
XX 61 LQKPGSPRLILYKYSNRFSGVDPDRFSGSGGTDFTLTKISRVAEDLGVYCYFGQTHAPY 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 LQKPGSPRLILYKYSNRFSGVDPDRFSGSGGTDFTLTKISRVAEDLGVYCYFGQTHAPY 120
XX
XX Db 61 LQKPGSPRLILYKYSNRFSGVDPDRFSGSGGTDFTLTKISRVAEDLGVYCYFGQTHAPY 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 121 TFGGKTLEIK-TAAAPSVFIFPPSDQLKSGTASVVCILNMFYPRKAVQMKVDNALQS 179
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 121 TFGGKTLEIKRTYAAPSVFIFPPSDQLKSGTASVVCILNMFYPRKAVQMKVDNALQS 180
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX 180 GNSQSVTEQSDSKSTVSLSTLTKSKADYEHKRYACEVTHQGLSSPYTSSFNRGEC 237
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 181 GNSQSVTEQSDSKSTVSLSTLTKSKADYEHKRYACEVTHQGLSSPYTSSFNRGEC 238
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX RESULT 6
XX ABR39842
XX ID ABR39842 standard; protein; 238 AA.
XX
XX ABR39842;
XX
XX 18-AUG-2003 (first entry)
XX
XX Humanised anti-Abeta antibody 266 light chain.
XX
XX Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
XX immunostimulant.
XX
XX Homo sapiens.
XX
XX WO2003016466-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US021322.
XX
XX 17-AUG-2001; 2001US-0313224P.
XX
XX (ELIL ) LILLY & CO ELL.
XX
XX Jia AY, Teuruehita N, Vaquez MJ;
XX
XX WPI: 2003-278557/27.
XX N-PSDB; ACC47226.
XX
XX New antibodies comprising a heavy chain and a light chain complementarily
XX determining regions from antibody 266, for treating and preventing
XX conditions associated with the A beta peptide, e.g. Alzheimer's disease
XX or Down syndrome.
XX
XX Disclosure; Fig 1; 82pp; English.
XX
XX The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
XX 266. The antibodies are useful for treating and preventing conditions
XX associated with the Abeta peptide, such as Alzheimer's disease, Down
XX syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
XX humans; for determining whether a human subject will respond to treatment
XX using humanized antibodies against Abeta; for treating, preventing and
XX reversing cognitive decline in clinical or pre-clinical Alzheimer's
XX disease. Down's syndrome or cerebral amyloid angiopathy; for inhibiting
XX formation of amyloid plaques of the effects of toxic soluble Abeta
XX species in humans. Treatment of the patients with antibody will inhibit
XX or prevent cognitive decline typically associated with disease
XX progression and reverses it. The present sequence represents a humanised
XX anti-Abeta antibody 266 light chain
XX
XX Sequence 238 AA;
XX
XX Query Match 90.4%; Score 1113.5; DB 6; Length 238;
XX Best Local Similarity 89.5%; Pred. No. 7.9e-62;
XX Matches 213; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
XX
XX 1 MCLPRLVLMFWIPASSSDVMTOTPLSLPVSIGDQASISCRSSQTIYHSNGNTLYEMV 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 MCLPRLVLMFWIPASSSDVMTOTPLSLPVSIGDQASISCRSSQTIYHSNGNTLYEMV 60
XX
XX 61 LQKPGSPRLILYKYSNRFSGVDPDRFSGSGGTDFTLTKISRVAEDLGVYCYFGQTHAPY 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 LQKPGSPRLILYKYSNRFSGVDPDRFSGSGGTDFTLTKISRVAEDLGVYCYFGQTHAPY 120
XX
XX Db 61 LQKPGSPRLILYKYSNRFSGVDPDRFSGSGGTDFTLTKISRVAEDLGVYCYFGQTHAPY 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


QY 121 TFGGSKLEIK-TAAPSVFIFPPSDDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQS 179
 DB 121 TFGGSKLEIKRTVAAPSVFIFPPSDDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQS 180
 QY 180 GNSQSSVTEQDSKSTYSLSSTLTLSKADYEKHKYIACGYTHOGISLPTPKSPNRGEC 237
 DB 181 GNSQSSVTEQDSKSTYSLSSTLTLSKADYEKHKYIACGYTHOGISLPTPKSPNRGEC 238

RESULT 7

ADS88785
 ID ADS88785 standard; protein; 238 AA.
 AC ADS88785;
 XX
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Sequence of the chimeric IC2 kappa light chain in M13mp19 clone M609.
 XX
 XX G glycoprotein; respiratory syncytial virus;
 KW respiratory syncytial virus infection; RSV; RSV infection; IC2; IgG1;
 KW chimeric.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Ig leader sequence"
 XX
 PN WO2004083373-A2.
 PD 30-SEP-2004.
 XX
 PF 22-MAR-2004; 2004WO-GB001239.
 XX
 PR 22-MAR-2003; 2003GB-00006618.
 XX
 PA (UNVE-) UNIV NEWCASTLE-UPON-TYNE.
 XX
 PI Toms G, Routledge B, Meksepralarad C;
 XX
 DR MPI; 2004-691033/67.
 DR N-PSDB; ADS88784.
 XX
 PF New antibody against the G glycoprotein of RSV with a variable region
 PT having a first and second domain from a VL and VH region, respectively,
 PT useful for treating respiratory syncytial virus (RSV) infections.
 PS Example 4; SEQ ID NO 55; 93bp; English.
 XX
 CC The specification describes an against the G glycoprotein of respiratory
 CC syncytial virus, with a variable region comprising a first domain from a
 CC variable light chain region and a second domain a variable heavy chain
 CC region. The antibodies of the invention are useful for treating and
 CC preventing the development of infections caused by the respiratory
 CC syncytial virus (RSV). The present sequence represents the chimeric IC2
 CC kappa light chain carried by pBE12 plasmid p533. IC2 is a murine
 CC monoclonal antibody known to bind to the RSV G glycoprotein. The above
 CC clone carries a mouse-human IgG1 chimeric antibody comprising IC2
 CC variable regions and human kappa light chain and gamma heavy chain
 CC constant regions.
 CC
 XX
 SQ Sequence 238 AA;

Query Match 89.8%; Score 1106; DB 8; Length 238;
 Best Local Similarity 91.8%; Pred. No. 2, 3e-61;
 Matches .214; Conservative 9; Mismatches 6; Indels 4; Gaps 2;

QY 9 VLMFPIPASS--SDVLTQTPLSLPSVSGDQASISCRSSQTTVHNGNTYLEWYLOKPG 65
 DB 6 ILFLVATRTGVSHDVLMTQTPLSLPVSIGDQASISCRSSQNTVHSDGNTYLEWYLOKPG 65

QY 66 QSPKLLIYKVNRFSGVDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGHAPYTFGGG 125
 DB 66 QSPKLLIYKVNRFSGVDRFSGSGSGSGTDFTLKISRVEAEDLGVYYCFQGHSHI PMTFGGG 125
 QY 126 TKLEIK-TAAPSVFIFPPSDDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQSGNSQE 184
 DB 126 TKLEIKRTVAAPSVFIFPPSDDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQSGNSQE 185
 QY 185 SVTEQDSKSTYSLSSTLTLSKADYEKHKYIACGYTHOGISLPTPKSPNRGEC 237
 DB 186 SVTEQDSKSTYSLSSTLTLSKADYEKHKYIACGYTHOGISLPTPKSPNRGEC 238

RESULT 8

ADP84971
 ID ADP84971 standard; protein; 219 AA.
 AC ADP84971;
 XX
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Chimeric antibody c1gG-Kar04.
 XX
 KW antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
 KW protease inhibitor; lectin; helix-bundle protein; lipocalin;
 KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;
 KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;
 KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
 KW metastasis.
 XX
 OS Mus musculus.
 XX
 PN WO2004050707-A2.
 PD 17-JUN-2004.
 XX
 PF 01-DEC-2003; 2003WO-DE003994.
 XX
 PR 29-NOV-2002; 2002DE-01056900.
 XX
 PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
 XX
 PI Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;
 PI Christensen PA;
 XX
 DR MPI; 2004-461095/43.
 XX
 PF New recognition molecules, e.g. antibodies (and nucleic acids) that bind
 PT specifically to Core-1 antigens, useful for diagnosis, treatment and
 PT prevention of tumors and metastases.
 PS Claim 26; SEQ ID NO 113; 136bp; German.
 XX
 CC This invention describes novel recognition molecules, especially
 CC antibodies that bind specifically to the Core-1 antigen. The recognition
 CC molecules are used to make constructs containing the framework regions
 CC where the framework regions are from the immunoglobulin (Ig) superfamily,
 CC where the framework regions are from the immunoglobulin (Ig) superfamily,
 CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.
 CC Most especially the framework regions are from antibodies, particularly
 CC the variable heavy chain (VH) and the variable light chain (VL) of human
 CC and/or murine origin. The constructs may also include a His or myc tag, a
 CC lysine-rich region and/or a multimerisation domain, most particularly it
 CC is a single-chain antibody fragment, multibody, Fab fragment, fusion
 CC protein of an antibody fragment with peptide or protein, and/or an Ig of
 CC types G, M, A, E or D and/or their subclasses. It may be human,
 CC humanised, murine or chimeric, e.g. IGM without the J chain. The
 CC additional sequences/structures in the constructs are Ig domains of
 CC various species, interacting or stabilising domains, signal sequences,
 CC fluorescent dyes, toxins, antibodies with catalytic activity or other
 CC specificities, cytolytic agents, enzymes, immuno-modulators or -
 CC effectors, MHC molecules, antigens, chelators for radioactive labels,

[illegible][illegible]

Db 61 YLQKQGSFRLIIYKVSNFSGVDPDRFSGSGSDTFTLKISRVEADVGVIYCSQSTHP 120
 QY 120 YTFGGGTLEIK-TAAPSVPFIPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
 Db 121 PAFGGGTKEIKRTVAAPSVPFIPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 180
 QY 179 SGNQGSSTVEDDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGRC 237
 Db 181 SGNQGSSTVEDDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGRC 239

RESULT 12

AA012915
 ID AAB12915 standard; protein; 239 AA.

AA012915;
 16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #82.

KM Antirheumatic agent; immunoglobulin M; Igm; apoptosis inducer;
 KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody.

OS Synthetic.

PN JP2000154149-A.

PD 06-JUN-2000.

PF 17-SEP-1999; 99JP-00263984.

PR 18-SEP-1998; 98JP-00264598.

XX (SANY) SANKYO CO LTD.

XX WPI; 2000-454476/40.

DR N-PSDB; AAA78269.

PT Anti-human Fas humanizing antibody-containing antirheumatic agents.

PS Claim 1; Page 70-71; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as
 CC active ingredients an immunoglobulin M (Igm) protein. The Igm protein
 CC does not include a J segment, has apoptosis inducing activity, and
 CC consists of a light and heavy chain polypeptide produced synthetically.
 CC The agents of the invention exhibit antirheumatic and immunosuppressive
 CC activity and can be used to treat autoimmune diseases, especially
 CC rheumatism. The Igm molecule used in the invention has human Fas-antigen
 CC binding properties. Included in the invention are nucleotide sequences of
 CC the Igm light and heavy chains (see AAA78267-A78272) and the
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
 CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
 CC chains used in the invention are represented by sequences AAA78213-
 CC A78266. Primers used for sequencing the human Ig DNA used in the
 CC invention are represented by sequences AAA78277-A78318 and AAA78335-
 CC A78337, while humanised anti-Fas Ig DNA sequencing primers are
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
 CC the production of the agent of the invention

XX Sequence 239 AA;

Query Match 88.6%; Score 1091; DB 3; Length 239;

Best Local Similarity 87.9%; Pred. No. 2e-60;
 Matches 210; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

QY 1 MKLPVRL-LVLMFWIPASSSDVIMTOTPLSLPVSLDQASISCRSQTIVHSNGNTYLEW 59

Db 1 MKLPQQLGLMLMWPFSSGDVVMQSPLSLPVTLAGQPASISCRSSKSLVHSNGNTYLEW 60
 QY 60 YLQKQGSFRLIIYKVSNFSGVDPDRFSGSGSDTFTLKISRVEADVGVIYCSQSTHAP 119
 Db 61 YLQKQGSFRLIIYKVSNFSGVDPDRFSGSGSDTFTLKISRVEADVGVIYCSQSTHP 120
 QY 120 YTFGGGTLEIK-TAAPSVPFIPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
 Db 121 PAFGGGTKEIKRTVAAPSVPFIPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 180
 QY 179 SGNQGSSTVEDDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGRC 237
 Db 181 SGNQGSSTVEDDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGRC 239

RESULT 13

AA071877
 ID AAW71877 standard; protein; 239 AA.

AA071877;
 18-JAN-1999 (first entry)

DE Anti-human Fas humanised antibody CH11 light chain VL-KF.

KM Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering.

OS Homo sapiens.

OS Synthetic.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

This is the amino acid sequence of a humanised anti-Fas antibody CH11

PF 28-JUN-2004; 2004WO-US020944.

XX

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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:47:53 ; Search time 21.3605 Seconds
(without alignments)
917.306 Million cell updates/sec

Title: US-10-828-782A-16

Perfect score: 1332
Sequence: 1 MKLPLRLVLMFWMIPASSD.....EVTHQGLSPVTKSFNRGEC 237

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1043	84.7	242	1 US-08-398-613A-56	Sequence 56, Appl
2	1043	84.7	242	1 US-08-398-612A-56	Sequence 56, Appl
3	1043	84.7	242	1 US-08-398-611A-56	Sequence 56, Appl
4	1043	84.7	242	1 US-08-491-334A-56	Sequence 56, Appl
5	1043	84.7	242	2 US-09-027-449-42	Sequence 42, Appl
6	1043	84.7	242	2 US-08-804-444A-42	Sequence 42, Appl
7	1043	84.7	242	2 US-09-026-985-42	Sequence 42, Appl
8	1043	84.7	242	2 US-09-121-952A-42	Sequence 42, Appl
9	1043	84.7	242	2 US-09-234-340A-42	Sequence 42, Appl
10	1043	84.7	242	2 US-09-355-014-42	Sequence 42, Appl
11	1029	83.5	239	2 US-08-487-550-6	Sequence 6, Appl
12	1029	83.5	239	2 US-09-526-098-6	Sequence 6, Appl
13	1029	83.5	239	2 US-09-383-916-6	Sequence 6, Appl
14	1029	83.5	239	2 US-09-758-173-6	Sequence 6, Appl
15	1029	83.5	239	2 US-09-576-424-6	Sequence 6, Appl
16	1015	82.4	239	2 US-10-000-489-8	Sequence 8, Appl
17	998.5	81.0	238	2 US-09-192-545-4	Sequence 8, Appl
18	978	79.4	238	2 US-09-698-705-10	Sequence 10, Appl
19	971	78.8	218	2 US-09-698-705-12	Sequence 12, Appl
20	963	78.2	242	2 US-09-027-449-51	Sequence 51, Appl
21	963	78.2	242	2 US-08-804-444A-51	Sequence 51, Appl
22	963	78.2	242	2 US-09-026-985-51	Sequence 51, Appl
23	963	78.2	242	2 US-09-121-952A-51	Sequence 51, Appl
24	963	78.2	242	2 US-09-234-340A-51	Sequence 51, Appl
25	963	78.2	242	2 US-09-355-014-51	Sequence 51, Appl
26	957	77.7	242	2 US-09-027-449-62	Sequence 62, Appl
27	957	77.7	242	2 US-09-026-985-62	Sequence 62, Appl

28	957	77.7	242	2 US-09-121-952A-62	Sequence 62, Appl
29	957	77.7	242	2 US-09-234-340A-62	Sequence 62, Appl
30	957	77.7	242	2 US-09-355-014-62	Sequence 62, Appl
31	955	77.5	242	2 US-09-027-449-56	Sequence 56, Appl
32	955	77.5	242	2 US-08-804-444A-56	Sequence 56, Appl
33	955	77.5	242	2 US-09-026-985-56	Sequence 56, Appl
34	955	77.5	242	2 US-09-121-952A-56	Sequence 56, Appl
35	955	77.5	242	2 US-09-234-340A-56	Sequence 56, Appl
36	955	77.5	242	2 US-09-355-014-56	Sequence 56, Appl
37	954.5	77.5	240	2 US-10-630-406-8	Sequence 8, Appl
38	951.5	77.2	219	2 US-09-027-449-72	Sequence 72, Appl
39	951.5	77.2	219	2 US-09-026-985-72	Sequence 72, Appl
40	951.5	77.2	219	2 US-09-121-952A-72	Sequence 72, Appl
41	951.5	77.2	219	2 US-09-234-340A-72	Sequence 72, Appl
42	951.5	77.2	219	2 US-09-355-014-72	Sequence 72, Appl
43	938	76.1	240	2 US-09-301-593-16	Sequence 36, Appl
44	932	75.6	241	1 US-07-916-098A-56	Sequence 56, Appl
45	923.5	75.0	239	2 US-09-627-896B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-398-613A-56
Sequence 56, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398, 613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fites, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874PI-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-398-613A-56
Query Match 84.7%; Score 1043; DB 1; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;
QY 7 LVLVLMFWMIPASS---SDVLTMTQTLPLSLVSGDQASISCRSSQRTIVHNGNVTYLEWYLOK 63

Db 8 L1ASFVFSIATNAVADIVMTQTPSLPVLSDQASISCRSSQSLVHGIGNTYLHMYLQK 67
Qy 64 PQOSPFLILYKYSNFSFSGVDPDRFSGSGSGTDFTLKISRVEADLGVYCFQGTAPYTFG 123
Db 68 PQOSPFLILYKYSNFSFSGVDPDRFSGSGSGTDFTLKISRVEADLGLYFCSGTHVPLTFG 127
Qy 124 GGTKEIKTA-AAPSVFIIPSPDEQLKSGTASVCLNFPYREAKVQKVNALQSGNS 182
Db 128 AGTKELKRAVAAPVFIIPSPSEQLKSGTASVCLNFPYREAKVQKVNALQSGNS 187
Qy 183 QESVTEQDSKSTYSLSTLTLSKADYEKHYACVTHQGLSPVTSFNRGEC 237
Db 188 QESVTEQDSKSTYSLSTLTLSKADYEKHYACVTHQGLSPVTSFNRGEC 242

RESULT 2

US-08-398-612A-56
Sequence 56, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: US/08/398,612A
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-612A-56

Query Match 84.7%; Score 1043; DB 1; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 L1AFMFWIPASS---SDVMTQTPSLPVLSDQASISCRSSQTIYHSNGNTLYEMYLQK 63
Db 8 L1ASFVFSIATNAVADIVMTQTPSLPVLSDQASISCRSSQSLVHGIGNTYLHMYLQK 67

Qy 64 PQOSPFLILYKYSNFSFSGVDPDRFSGSGSGTDFTLKISRVEADLGVYCFQGTAPYTFG 123
Db 68 PQOSPFLILYKYSNFSFSGVDPDRFSGSGSGTDFTLKISRVEADLGLYFCSGTHVPLTFG 127
Qy 124 GGTKEIKTA-AAPSVFIIPSPDEQLKSGTASVCLNFPYREAKVQKVNALQSGNS 182
Db 128 AGTKELKRAVAAPVFIIPSPSEQLKSGTASVCLNFPYREAKVQKVNALQSGNS 187
Qy 183 QESVTEQDSKSTYSLSTLTLSKADYEKHYACVTHQGLSPVTSFNRGEC 237
Db 188 QESVTEQDSKSTYSLSTLTLSKADYEKHYACVTHQGLSPVTSFNRGEC 242

RESULT 3

US-08-398-611A-56
Sequence 56, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
TITLE OF INVENTION: Of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: US/08/398,611A
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-611A-56

Query Match 84.7%; Score 1043; DB 1; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 L1AFMFWIPASS---SDVMTQTPSLPVLSDQASISCRSSQTIYHSNGNTLYEMYLQK 63
Db 8 L1ASFVFSIATNAVADIVMTQTPSLPVLSDQASISCRSSQSLVHGIGNTYLHMYLQK 67
Qy 64 PQOSPFLILYKYSNFSFSGVDPDRFSGSGSGTDFTLKISRVEADLGVYCFQGTAPYTFG 123
Db 68 PQOSPFLILYKYSNFSFSGVDPDRFSGSGSGTDFTLKISRVEADLGLYFCSGTHVPLTFG 127
Qy 124 GGTKEIKTA-AAPSVFIIPSPDEQLKSGTASVCLNFPYREAKVQKVNALQSGNS 182

Db 128 AGTKLELRAVAAPVFIFFPPSSSEQLKSGTASVVCCLNNFYPREAKVOMKVDNALQSGNS 187
Qy 183 QESVTEODSKOSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTSFNRGEC 237
Db 188 QESVTEODSKOSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTSFNRGEC 242

RESULT 4

US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; TITLE OF INVENTION: Disorders and Asthma
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491.334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P2
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-491-334A-56

Query Match 84.7%; Score 1043; DB 1; Length 242;

Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 LLYVMFWIPASS---SDVLTMTOTPLSLPVSLGDQASISCRSSQTLVHNGNTLYEMWYLOK 63
Db 8 LLAASFVFSIATNAYADIVMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLMWYLOK 67
Qy 64 PGQSPKLLIYKSNRFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYVCFQGTTHAPYTFG 123
Db 68 PGQSPKLLIYKSNRFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYVCFQGTTHAPYTFG 127
Qy 124 GGTGLEIKTA-AAPSVFIFFPPSDEQLKSGTASVVCCLNNFYPREAKVOMKVDNALQSGNS 182
Db 128 AGTKLELRAVAAPVFIFFPPSSEQLKSGTASVVCCLNNFYPREAKVOMKVDNALQSGNS 187
Qy 183 QESVTEODSKOSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTSFNRGEC 237

Db 188 QESVTEODSKOSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTSFNRGEC 242

RESULT 5

US-09-027-449-42
; Sequence 42, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027.449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P108SR3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-42

Query Match 84.7%; Score 1043; DB 2; Length 242;

Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 LLYVMFWIPASS---SDVLTMTOTPLSLPVSLGDQASISCRSSQTLVHNGNTLYEMWYLOK 63
Db 8 LLAASFVFSIATNAYADIVMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLMWYLOK 67
Qy 64 PGQSPKLLIYKSNRFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYVCFQGTTHAPYTFG 123
Db 68 PGQSPKLLIYKSNRFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYVCFQGTTHAPYTFG 127
Qy 124 GGTGLEIKTA-AAPSVFIFFPPSDEQLKSGTASVVCCLNNFYPREAKVOMKVDNALQSGNS 182
Db 128 AGTKLELRAVAAPVFIFFPPSSEQLKSGTASVVCCLNNFYPREAKVOMKVDNALQSGNS 187
Qy 183 QESVTEODSKOSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTSFNRGEC 237
Db 188 QESVTEODSKOSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTSFNRGEC 242

RESULT 6

```

US-08-804-444A-42
/ Sequence 42, Application US/0880444A
/ Patent No. 6117980
/ GENERAL INFORMATION:
/ APPLICANT: Gonzalez, Tania N
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/804,444A
/ FILING DATE: 21-Feb-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5530
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 242 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
US-08-804-444A-42

Query Match      84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6,5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LILVIMFWIPASS--SDVIMTQTPLSLPVSLGDQASISCRSSQTIIVHSNGNTYLEMYLQK 63
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 8 ILASWFVSIATNAYADIYMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLMYLOK 67
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 PQOSPRLILYKSNRFSGVPRDFSGSGSTDTFTLIRISVEADLGIYFCOSSTHVPFLTFG 123
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 68 PQOSPRLILYKSNRFSGVPRDFSGSGSTDTFTLIRISVEADLGIYFCOSSTHVPFLTFG 127
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 GGTKEIKTA-AAPSVFIPEPDEQKSGTASVCLNNFYPREAKVQKVNALQSGNS 182
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 128 AGTKELKRAVAAPVFIPEPSEQKSGTASVCLNNFYPREAKVQKVNALQSGNS 187
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 QESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSPVTKSFNRGEC 237
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 188 QESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSPVTKSFNRGEC 242
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-09-026-985-42
/ Sequence 42, Application US/09026985
/ Patent No. 6133426
/ GENERAL INFORMATION:
/ APPLICANT: Gonzalez, Tania R.
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
/ TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 72
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Genentech, Inc.

```

```

/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/026,985
/ FILING DATE: 20-Feb-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085R3-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5530
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 242 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
US-09-026-985-42

Query Match      84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6,5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LILVIMFWIPASS--SDVIMTQTPLSLPVSLGDQASISCRSSQTIIVHSNGNTYLEMYLQK 63
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 8 ILASWFVSIATNAYADIYMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLMYLOK 67
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 PQOSPRLILYKSNRFSGVPRDFSGSGSTDTFTLIRISVEADLGIYFCOSSTHVPFLTFG 123
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 68 PQOSPRLILYKSNRFSGVPRDFSGSGSTDTFTLIRISVEADLGIYFCOSSTHVPFLTFG 127
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 GGTKEIKTA-AAPSVFIPEPDEQKSGTASVCLNNFYPREAKVQKVNALQSGNS 182
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 128 AGTKELKRAVAAPVFIPEPSEQKSGTASVCLNNFYPREAKVQKVNALQSGNS 187
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 QESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSPVTKSFNRGEC 237
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 188 QESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSPVTKSFNRGEC 242
   |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-09-121-952A-42
/ Sequence 42, Application US/09121952A
/ Patent No. 6458355
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc., Hsei, Vanessa
/ APPLICANT: Koumenis, Iphigenia
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Shakhoh, Zahra
/ APPLICANT: Zapata, Gerardo A.
/ TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
/ TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
/ NUMBER OF SEQUENCES: 72
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ OPERATING SYSTEM: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-JUL-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-42

Query Match 84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LVLVFWIPASS---SDVLTMTQTPSLPVSIGDQASISCRSSQRTVHSGNWTYLEMYLQK 63
DB 8 LLASMFVSINMTNADIVMTQTPSLPVSIGDQASISCRSSQSLVHGIGMTYLYLHWYLOK 67
QY 64 PGQSPKLLIYVSNRFSQVDPDRFSGSGGSDTFTLKISVEAEADLGVYCFQGTAPYTFG 123
DB 68 PGQSPKLLIYVSNRFSQVDPDRFSGSGGSDTFTLRISVEAEADLGVYCFQGTAPYTFG 127
QY 124 GGTLEIKETA--AASVVFIFPPPSDEOLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 182
DB 128 AGTKLELRRAVAAPVFIFFPPSSSQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 187
QY 183 QESVTEQDSKQSTYSLSTLTLSKADYEKKYVACEVTHQGLSSPVTSGFNRGEC 237
DB 188 QESVTEQDSKQSTYSLSTLTLSKADYEKKYVACEVTHQGLSSPVTSGFNRGEC 242

RESULT 9
US-09-234-340A-42
Sequence 42, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., HseI, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-JUL-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-42

Query Match 84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LVLVFWIPASS---SDVLTMTQTPSLPVSIGDQASISCRSSQRTVHSGNWTYLEMYLQK 63
DB 8 LLASMFVSINMTNADIVMTQTPSLPVSIGDQASISCRSSQSLVHGIGMTYLYLHWYLOK 67
QY 64 PGQSPKLLIYVSNRFSQVDPDRFSGSGGSDTFTLKISVEAEADLGVYCFQGTAPYTFG 123
DB 68 PGQSPKLLIYVSNRFSQVDPDRFSGSGGSDTFTLRISVEAEADLGVYCFQGTAPYTFG 127
QY 124 GGTLEIKETA--AASVVFIFPPPSDEOLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 182
DB 128 AGTKLELRRAVAAPVFIFFPPSSSQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 187
QY 183 QESVTEQDSKQSTYSLSTLTLSKADYEKKYVACEVTHQGLSSPVTSGFNRGEC 237
DB 188 QESVTEQDSKQSTYSLSTLTLSKADYEKKYVACEVTHQGLSSPVTSGFNRGEC 242

RESULT 10
US-09-355-014-42
Sequence 42, Application US/09355014
Patent No. 6670033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., HseI, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-355-014-42
Query Match 84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;
QY 7 LLYVFWIRASS---SDVMTQTPLSLPVSIGDQASISCRSSQTIYHSGNTYLEMYLQK 63
DB 8 LLASMEVFSLATNANADIVTQTPLSLPVSLGDQASISCRSSQSLVHGNTYLLHWYLOK 67
QY 64 PQOSPFLILYKVNRSRSGVDFRPSGSGGDTFTLKISRYEADLVGYVCGGTHAPYTPG 123
DB 68 PQOSPFLILYKVNRSRSGVDFRPSGSGGDTFTLKISRYEADLVGYVCGGTHAPYTPG 127
QY 124 GGTLEIKTA-AAPSVFIFFPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSGNS 182
DB 128 AGTKLELKAVALPVTFFIPPSSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNS 187
QY 183 QSSVTEQDSKSTYSLSSTLTLSKADYEKHYACVTHQGLSPVTKSFNRGEC 237
DB 188 QSSVTEQDSKSTYSLSSTLTLSKADYEKHYACVTHQGLSPVTKSFNRGEC 242
RESULT 11
US-08-487-550-6
Sequence 6, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-6
Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;
QY 1 MGLPVRL-LVMEFWIPASSDYLMQTPLSLPVSIGDQASISCRSSQTIYHSGNTYLEM 59
DB 1 MSLPAQLGLILLCLVPGSSGGRVVMQSPISLPTGEPASISCRSSQSLKSHNGTFLSM 60
QY 60 YLQKPGSPKLLIYKVNRSRSGVDFRPSGSGGDTFTLKISRYEADLVGYVCGGTHAP 119
DB 61 YQKPGQPPRLIYKVNRSRSGVDFRPSGSGGDTFTLKISRYEADLVGYVCGGTHAP 120
QY 120 YTFGGGTLEIK-TAAPSVFIFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQ 178
DB 121 PTFGGGTVEIKRTYAAPSVFIFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQ 180
QY 179 SGNQSESVTEQDSKSTYSLSSTLTLSKADYEKHYACVTHQGLSPVTKSFNRGEC 237
DB 181 SGNQSESVTEQDSKSTYSLSSTLTLSKADYEKHYACVTHQGLSPVTKSFNRGEC 239
RESULT 12
US-09-526-098-6
Sequence 6, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-6

Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MKLPLRLI-VLMFPIPASSSDVLTMTQPLSLPVSLGDQASISCRSSQTIHNSNGTYLIEW 59
DB 1 MSLLPAQLLGLLLCVPGSSGEVVMQTQSLPIITPGEPAISICRSSQSLKHSNGDTFLSW 60
QY 60 YLQKPGSPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCFQGTAP 119
DB 61 YQKRGQPPRLIYKVSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCQGTTRTP 120
QY 120 YTFGGGTLEIK-TRAAPSVFIPEPSDEQLKSGTASVCLINNFYPREAKYQWKVDNALQ 178
DB 121 PTFGGGTVEIKRTVAAPSVFIPEPSDEQLKSGTASVCLINNFYPREAKYQWKVDNALQ 180
QY 179 SGNQSESTVEDSDKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGEC 237
DB 181 SGNQSESTVEDSDKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGEC 239

RESULT 13

US-09-383-916-6
Sequence 6, Application US/09383916
Patent No. 6709654

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-6

Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MKLPLRLI-VLMFPIPASSSDVLTMTQPLSLPVSLGDQASISCRSSQTIHNSNGTYLIEW 59
DB 1 MSLLPAQLLGLLLCVPGSSGEVVMQTQSLPIITPGEPAISICRSSQSLKHSNGDTFLSW 60
QY 60 YLQKPGSPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCFQGTAP 119
DB 61 YQKRGQPPRLIYKVSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCQGTTRTP 120
QY 120 YTFGGGTLEIK-TRAAPSVFIPEPSDEQLKSGTASVCLINNFYPREAKYQWKVDNALQ 178
DB 121 PTFGGGTVEIKRTVAAPSVFIPEPSDEQLKSGTASVCLINNFYPREAKYQWKVDNALQ 180
QY 179 SGNQSESTVEDSDKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGEC 237
DB 181 SGNQSESTVEDSDKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGEC 239

RESULT 14

US-09-758-173-6
Sequence 6, Application US/09758173
Patent No. 6893638

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,173
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-758-173-6

Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MKLPLRLI-VLMFPIPASSSDVLTMTQPLSLPVSLGDQASISCRSSQTIHNSNGTYLIEW 59
DB 1 MSLLPAQLLGLLLCVPGSSGEVVMQTQSLPIITPGEPAISICRSSQSLKHSNGDTFLSW 60

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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:37:39 ; Search time 153.339 Seconds
(without alignments)
1323.818 Million cell updates/sec

Title: US-10-828-782A-18
Perfect score: 2450
Sequence: 1 MECSVMFLFSLGTAVLSE.....MHKALHNYTKSLSLSPGK 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2490	100.0	462	ADU70079	Adu70079 Mouse/hum
2	2174	87.3	470	AAU74296	Aau74296 Anti-huma
3	2172.5	87.2	471	AD828427	Ad828427 Human ant
4	2170.5	87.2	463	AAW14939	Aaw14939 3F4 (Chim
5	2170.5	87.2	463	AAW14940	Aaw14940 3F4 (Chim
6	2153	86.5	464	AEA41032	Aea41032 Human ant
7	2146	86.2	462	AD257693	Ad257693 Anti-cMet
8	2145.5	86.2	466	ADTS1705	Adts1705 Vls11izum
9	2143.5	86.1	442	ADTS1693	Adts1693 Dac11izum
10	2143.5	86.1	469	AEBA5869	Aeba5869 Human mon
11	2142.5	86.0	446	ADTS1703	Adts1703 Vls11izum
12	2142.5	86.0	446	ADTS1704	Adts1704 Vls11izum
13	2140.5	86.0	442	ADTS1692	Adts1692 Dac11izum
14	2140.5	86.0	442	ADTS1691	Adts1691 Dac11izum
15	2139.5	85.9	446	ADTS1706	Adts1706 Vls11izum
16	2137.5	85.8	442	ADTS1694	Adts1694 Dac11izum
17	2137.5	85.8	446	ADTS1707	Adts1707 Vls11izum
18	2137.5	85.8	469	AEBA5877	Aeba5877 Human mon
19	2135.5	85.8	442	ADTS1695	Adts1695 Dac11izum
20	2135.5	85.8	450	AEBA2321	Aeba2321 Anti-TRK
21	2128	85.5	472	AAV50157	Aav50157 Chimeric
22	2127.5	85.4	461	AAW72236	Aaw72236 Humanised
23	2108	84.7	445	ADKS2332	Adks2332 Human ant
24	2108	84.7	462	AAW14933	Aaw14933 2A2 (Chim

25	2108	84.7	462	2	AAW14934	Aaw14934 2A2 (Chim
26	2107	84.6	445	8	ADKS2312	Adks2312 Human ant
27	2105	84.5	445	8	ADKS2384	Adks2384 Human ant
28	2103.5	84.5	450	2	AAW34505	Aaw34505 Heavy cha
29	2103.5	84.5	450	2	AAV08755	Aav08755 Heavy Igg
30	2103.5	84.5	450	5	AEGB31890	Aegb31890 Full leng
31	2103.5	84.5	450	8	ADK18343	Adk18343 Amino aci
32	2103	84.5	445	8	ADKS2296	Adks2296 Human ant
33	2090.5	84.0	552	2	AAK30775	Aak30775 PH52-8.0
34	2089.5	83.9	463	8	ADMA4569	Adma4569 Anti-inte
35	2088	83.9	462	2	AD257705	Ad257705 Anti-cMet
36	2088	83.9	464	8	ADU68011	Adu68011 Mouse ant
37	2087	83.8	470	8	ADM72027	Adm72027 Chimeric
38	2086	83.8	468	9	ADV92468	Adv92468 SMS-1 chi
39	2086	83.8	468	9	ADV98531	Adv98531 Novel chi
40	2086	83.8	624	9	ADV92486	Adv92486 chSMV/Rc
41	2086	83.8	624	9	ADV98549	Adv98549 Novel chi
42	2086	83.8	639	9	ADV92488	Adv92488 chSMV/Rc
43	2086	83.8	639	9	ADV98551	Adv98551 Novel chi
44	2085	83.7	470	5	AAE27923	Aae27923 Human C2B
45	2085	83.7	470	6	ABB82832	Abb82832 Antibody

ALIGNMENTS

RESULT 1	ADU70079	ADU70079 standard; protein; 462 AA.
XX	ADU70079;	
AC	ADU70079;	
XX	ADU70079;	
DT	24-FEB-2005 (first entry)	
DE	Mouse/human chimeric monoclonal antibody 6B5 heavy chain, SEQ:18.	
XX	Antibody engineering; chimeric antibody; drug dependence; phenacylidine;	
XX	PCP; antidiabetic; toxicity; toxicity and intoxication;	
KW	psychiatric disorder; immunoglobulin; chimeric monoclonal antibody 6B5;	
KM	ch-mabB5; heavy chain.	
XX	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
PN	US2004242848-A1.	
XX	02-DEC-2004.	
PD	21-APR-2004; 2004US-00828782.	
PF	21-APR-2003; 2003US-0464190P.	
PR	(OWEN/) OWENS S M.	
PA	(LACY/) LACY H M.	
XX	Owens SM, Lacy HM;	
PI	WPI, 2005-011672/01.	
DR	N-Psdb; ADU70078.	
XX	New chimeric mouse/human monoclonal antibody for treating phenacylidine	
PT	drug abuse and toxicity comprises human immunoglobulin constant domains	
PT	and immunoglobulin variable domains of murine antibody.	
XX	Claim 6; SEQ ID NO 18; 34pp; English.	
XX	The invention relates to a chimeric mouse/human monoclonal antibody named	
CC	ch-mabB5 (see ADU70077 and ADU70079) which is specific for phenacylidine	
CC	(PCP). ch-mabB5 comprises immunoglobulin constant domains of human	
CC	origin and immunoglobulin variable domains from the murine anti-PCP	
CC	monoclonal antibody 6B5. The invention also relates to DNA sequences	
CC	encoding the light and heavy chains of the chimeric antibody (ADU70076	

Db 241 TVERKCCVECPCPAPVAGPSVFLPPKPKDTLMSRTPEVTCVVDVSHEDPEVQPN 300
 QY 293 YVDGVEVHNAKTPREBQFNSTFRVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTIS 352
 Db 301 YVDGVEVHNAKTPREBQFNSTFRVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTIS 360
 QY 353 KTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTPM 412
 Db 361 KTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTPM 420
 QY 413 LDDSGSFLLYSKLTVDKSRMOQGNVSCSVMEHALHNHYTKSLSLSPGK 462
 Db 421 LDDSGSFLLYSKLTVDKSRMOQGNVSCSVMEHALHNHYTKSLSLSPGK 470
 Db 421 LDDSGSFLLYSKLTVDKSRMOQGNVSCSVMEHALHNHYTKSLSLSPGK 470
 RESULT 3
 ADE28427
 ID ADE28427 standard; protein; 471 AA.
 AC ADE28427;
 XX 29-JAN-2004 (first entry)
 DE Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.
 XX anti-CD40 monoclonal antibody; CD40; cytosolic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; variable region heavy chain; 21-2-1.
 XX Homo sapiens.
 OS
 XX MO2003040170-A2.
 PN 15-MAY-2003.
 XX 08-NOV-2002; 2002WO-US036107.
 PF 09-NOV-2001; 2001US-0348980P.
 PR (PRIZ) PRIZER PROD INC.
 PA (ABGE-) ABGENIX INC.
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 PI WPI; 2003-441521/41.
 XX N-PSDB; ADE28426.
 DR New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.
 PS Claim 1; SEQ ID NO 34; 177pp; English.
 XX The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytosolic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region heavy chain protein of the invention.
 XX Sequence 471 AA;
 SQ Query Match 87.2%; Score 2172.5; DB 7; Length 471;
 Best Local Similarity 86.2%; Pred. No. 4.8e-123;
 Matches 406; Conservative 23; Mismatches 33; Indels 9; Gaps 1;

QY 1 MECSGCVMLFLLSGTAGVLSVVOLOQSGBELVKGASVVMSCSKASGYTGTDYIIHMKQSH 60
 Db 1 MDMTWRLIFLVAAGTAHSGVQLVQSGAEVKKPGASGVYSCKASGYTFTGYMHVRQAP 60
 QY 61 GKSLFEMIGYIYFNNGNGYNKQEPKQKATLTVDKSSSTYMLRLITLSDSAVYYGR--- 117
 Db 61 GQGLEMMGMWIMPDGSGTNYAQKFGQRYMTDTISIAYMEILNRLRSDTAVYYCARQDP 120
 QY 118 -----STWDDFDWMGGGTTLTVSASSTKGPSVPLAPCSSTSESTAALGLVVDYRPE 171
 Db 121 LGYCTNGVCSYFDWVGQGLTVTVSSASTKGPSVPLAPCSSTSESTAALGLVVDYRPE 180
 QY 172 PVTVSNSGALTSGVHTFPAVLQSSGLYSLSVTVPSNSFGTQTYTCNVDHKSNTKYD 231
 Db 181 PVTVSNSGALTSGVHTFPAVLQSSGLYSLSVTVPSNSFGTQTYTCNVDHKSNTKYD 240
 QY 232 KTVERRKCCVECPCPAPVAGPSVFLPPKPKDTLMSRTPEVTCVVDVSHEDPEVQPN 291
 Db 241 KTVERRKCCVECPCPAPVAGPSVFLPPKPKDTLMSRTPEVTCVVDVSHEDPEVQPN 300
 QY 292 WYVDGVEVHNAKTPREBQFNSTFRVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTIS 351
 Db 301 WYVDGVEVHNAKTPREBQFNSTFRVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTIS 360
 QY 352 SKTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 411
 Db 361 SKTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 420
 QY 412 MLDDSGSFLLYSKLTVDKSRMOQGNVSCSVMEHALHNHYTKSLSLSPGK 462
 Db 421 MLDDSGSFLLYSKLTVDKSRMOQGNVSCSVMEHALHNHYTKSLSLSPGK 471
 RESULT 4
 AAW14939
 ID AAW14939 standard; protein; 463 AA.
 AC AAW14939;
 XX 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX 3F4 (Chimeric) human G2/G4 chimeric antibody.
 DE Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAW; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX Homo; sapiens.
 OS Mus sp.
 OS Chimeric.
 XX WO9711971-A1.
 PN 03-APR-1997.
 PD 27-SEP-1996; 96WO-US015575.
 PF 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX (ALEX-) ALEXION PHARM INC.
 PA Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;
 PI WPI; 1997-212855/19.
 XX N-PSDB; AAT62936.
 DR Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 XX Disclosure; Page 56-57; 105pp; English.

XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see
 CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs into
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 463 AA;

Query Match 87.2%; Score 2170.5; DB 2; Length 463;

Beat Local Similarity 88.1%; Pred. No. 6.2e-123; Matches 408; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 MECSQVFLSLSTAGTAVSEVQLQSGPELVKPGASVKMSCKASGVTGTDYIIMMKQSH 60
 DB 1 MKMSVILFLSLVTAGVSHQVQVQSGAEIAPMAVSILSKASGYNFNSYMQVVKQRP 60
 QY 61 GKSLFMIGIYIPNNGNGYNGQFKGKATLTVDKSSSTAYMEIRTLTSEDSAVYYCGRTW 120
 DB 61 GQGLEMIGAIYPGDDTSTYQKFRKATLTADKSSSTAYMQLSLASDSAVYYCARRTV 120
 QY 121 DD-FPYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSMNS 179
 DB 121 GGYFPMYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSMNS 180
 QY 180 GALTSGVHTFPAVLOSGGLYSLSVTVTPSSNFGQTYTCNVDHPSNTKVDTERKCC 239
 DB 181 GALTSGVHTFPAVLOSGGLYSLSVTVTPSSNFGQTYTCNVDHPSNTKVDTERKCC 240
 QY 240 VECPCPAPVAVGSPVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVQFMYYDGVGV 299
 DB 241 VECPCPAPVAVGSPVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVQFMYYDGVGV 300
 QY 300 HNAKTKPREBOFNSTFRVSVTLTVHODMLNGEKYCKVSNKGLPAPIEKTIISKTKGQPR 359
 DB 301 HNAKTKPREBOFNSTFRVSVTLTVHODMLNGEKYCKVSNKGLPAPIEKTIISKTKGQPR 360
 QY 360 EPOVYTLTPSRREMTKNQVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPMLDSDGSF 419
 DB 361 EPOVYTLTPSRREMTKNQVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPMLDSDGSF 420
 QY 420 FLYSKLTVDKSRMQGNVFSQVMEBALHNHYTQSLSLSPCK 462
 DB 421 FLYSKLTVDKSRMQGNVFSQVMEBALHNHYTQSLSLSPCK 463

RESULT 5
 AAW14940 standard; protein; 463 AA.

XX AAW14940;
 AC AAW14940;
 XX 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX 3F4 (Chimeric) human G2/G4 chimeric antibody.
 DB Xenotransplantation; graft rejection; cell interaction; pig;
 XX vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX Homo; sapiens.
 OS Mus sp.
 OS Chimeric.
 XX WO9711971-A1.
 XX 03-APR-1997.
 PD 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.
 PR 26-SEP-1996; 96US-00004489.
 XX (ALEX-) ALEXION PHARM INC.
 PA Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matris LA;
 PI WPI; 1997-212855/19.
 DR N-PsDB; AAT62937.
 XX Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 PS Disclosure; Page 58-61, 105pp; English.

QY 1 MECSQVFLSLSTAGTAVSEVQLQSGPELVKPGASVKMSCKASGVTGTDYIIMMKQSH 60
 DB 1 MKMSVILFLSLVTAGVSHQVQVQSGAEIAPMAVSILSKASGYNFNSYMQVVKQRP 60
 QY 61 GKSLFMIGIYIPNNGNGYNGQFKGKATLTVDKSSSTAYMEIRTLTSEDSAVYYCGRTW 120
 DB 61 GQGLEMIGAIYPGDDTSTYQKFRKATLTADKSSSTAYMQLSLASDSAVYYCARRTV 120
 QY 121 DD-FPYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSMNS 179
 DB 121 GGYFPMYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSMNS 180
 QY 180 GALTSGVHTFPAVLOSGGLYSLSVTVTPSSNFGQTYTCNVDHPSNTKVDTERKCC 239
 DB 181 GALTSGVHTFPAVLOSGGLYSLSVTVTPSSNFGQTYTCNVDHPSNTKVDTERKCC 240
 QY 240 VECPCPAPVAVGSPVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVQFMYYDGVGV 299
 DB 241 VECPCPAPVAVGSPVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVQFMYYDGVGV 300
 QY 300 HNAKTKPREBOFNSTFRVSVTLTVHODMLNGEKYCKVSNKGLPAPIEKTIISKTKGQPR 359
 DB 301 HNAKTKPREBOFNSTFRVSVTLTVHODMLNGEKYCKVSNKGLPAPIEKTIISKTKGQPR 360
 QY 360 EPOVYTLTPSRREMTKNQVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPMLDSDGSF 419
 DB 361 EPOVYTLTPSRREMTKNQVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPMLDSDGSF 420
 QY 420 FLYSKLTVDKSRMQGNVFSQVMEBALHNHYTQSLSLSPCK 462
 DB 421 FLYSKLTVDKSRMQGNVFSQVMEBALHNHYTQSLSLSPCK 463

RESULT 6
 AEA41032 standard; protein; 464 AA.

XX AEA41032;
 AC AEA41032;
 XX 28-JUL-2005 (first entry)
 DT 28-SEP-1996; 96WO-US015575.

DE Human anti-M-CSF antibody 1.120.1 heavy chain protein SEQ ID NO:22.
 XX monoclonal antibody; macrophage colony stimulating factor inhibition;
 KW antitumor; antiproliferative; antirheumatic; antiviral; antibacterial;
 KW immunosuppressive; neuroprotective; nocotropic; cerebroprotective;
 KW vasodilator; cytoskeletal; antiproliferative; respiratory-gen.; antimetabolic;
 KW arthritis; psoriatic arthritis; rheumatoid arthritis; gout; sepsis;
 KW septic shock; endotoxic shock; Alzheimer's disease;
 KW cerebrovascular ischemia; asthma; respiratory distress syndrome;
 KW cerebral malaria; tumor; heavy chain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1..19
 FT Peptide /label= signal
 FT 20..464
 FT Protein /note= "human anti-M-CSF antibody 1.120.1 heavy chain"
 FT 20..139
 FT Domain /note= variable domain
 FT 45..54
 FT Region /note= "complementarity determining region CDR1"
 FT 69..85
 FT Region /note= "complementarity determining region CDR2"
 FT 118..127
 FT Region /note= "complementarity determining region CDR3"
 FT 140..464
 FT Domain /note= constant domain
 FT
 XX GB2405873-A.
 XX 16-MAR-2005.
 XX
 PD 09-SEP-2004; 2004GB-00020044.
 XX
 PF 10-SEP-2003; 2003US-0502163P.
 XX
 PR (WARNER) WARNER LAMBERT CO LLC.
 XX (ABGE-) ABGENIX INC.
 PA
 XX Bedian V, Devalaraja MN, Low JE, Mobley JL, Kellermann S;
 PI Poltz I, Haak-Frendescho M;
 PI WPI: 2005-216576/23.
 DR
 XX Novel humanized, chimeric or human monoclonal antibody e.g. 9.14.41 or
 PT 8.10.3F antibody that binds to and inhibits human macrophage colony
 PT stimulating factor, useful for producing medicament for treating
 PT rheumatoid arthritis.
 XX
 PS Claim 6; SEQ ID NO 22; 155BP; English.
 XX
 CC The invention relates to a humanized, chimeric or human monoclonal
 CC antibody (I) or its antigen-binding portion that binds specifically to
 CC and inhibits human macrophage colony stimulating factor (M-CSF). Also
 CC described: (1) a polypeptide chosen from AEA41017, AEA41019, AEA41021,
 CC AEA41033, AEA41035, AEA41037, AEA41039, AEA41041, AEA41043, AEA41045,
 CC AEA41047, AEA41049, AEA41051, AEA41053, AEA41054, AEA41056,
 CC AEA41057, AEA41058, AEA41059, AEA41060, AEA41061, AEA41062, AEA41063,
 CC AEA41064, AEA41065, AEA41066, AEA41067 and AEA41068, without a signal
 CC sequence; (2) a composition (II) comprising (I) and a carrier; (3) an
 CC isolated cell line (III) for producing (I) or its antigen-binding portion
 CC or heavy or light chain of (I) or antigen-binding portions; and (4)
 CC producing (I). (I) is useful for producing a medicament for treating a
 CC condition chosen from arthritis, psoriatic arthritis, rheumatoid
 CC arthritis, gout, traumatic arthritis, rubella arthritis and acute
 CC synovitis and other arthritic conditions, sepsis, septic shock, endotoxic
 CC shock, gram negative sepsis, toxic shock syndrome, Alzheimer's disease,
 CC stroke, neurotrauma, asthma, adult respiratory distress syndrome,
 CC cerebral malaria, tumor, and chronic pulmonary inflammatory disease,
 CC preferably rheumatoid arthritis. The present sequence represents the

CC human anti-M-CSF antibody 1.120.1 heavy chain, which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 464 AA;
 XX
 Query Match 86.5%; Score 2153; DB 9; Length 464;
 Best Local Similarity 86.9%; Pred. No. 7.1e-122;
 Matches 403; Conservative 23; Mismatches 36; Indels 2; Gaps 1;
 QY 1 MECSQVMEFLISGTVLSEVQLOQSGPELVKPGASVMSKCSGASGTGTDYIHMMKQSH 60
 DB 1 MEWTSFLFLVAATGASHQVQLVQSGAEVKKPGASVAVSCASGYTTSYGIISWRQNP 60
 QY 61 GKSLEWIGYIVPNNGNGYNGKFKGATLTVDKSSSTAYMELRTTSEDAVYVYGRSTW 120
 DB 61 GQGLEWGMWISAYNGNTMYAQKLDQRYMTTDTSTTAYMELRSLSDDTAVYVYCARRY 120
 QY 121 --DDFDVWGQGTTLTVSSASSTKGPSVFPPLAPCSRSSTSTALGCLVXDYFPEPTVSN 178
 DB 121 GANFPDYGQGTLLTVSSASSTKGPSVFPPLAPCSRSSTSTALGCLVXDYFPEPTVSN 180
 QY 179 SGALTSGVHTTPAVLQSSGLYSLSVTVVPSNFGTQTYTCNVHDKPSNTKYDKVERKC 238
 DB 181 SGALTSGVHTTPAVLQSSGLYSLSVTVVPSNFGTQTYTCNVHDKPSNTKYDKVERKC 240
 QY 239 CVECPPCAPPAVAGSVFLPPKPKDMLMISRTPEVTCNVVDVSHEDPEVQNMVYDVG 298
 DB 241 CVECPPCAPPAVAGSVFLPPKPKDMLMISRTPEVTCNVVDVSHEDPEVQNMVYDVG 300
 QY 299 VHNATKPREBQPNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGP 358
 DB 301 VHNATKPREBQPNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGP 360
 QY 359 REPQYTYLPFSREBETKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPMLDSQGS 418
 DB 361 REPQYTYLPFSREBETKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPMLDSQGS 420
 QY 419 FFLYSKLTVDKSRMQQGNVPSGVHBAIHHNYTOKSLSLSPGK 462
 DB 421 FFLYSKLTVDKSRMQQGNVPSGVHBAIHHNYTOKSLSLSPGK 464
 XX
 XX RESULT 7
 XX AD257693
 XX ID AD257693 standard; protein; 462 AA.
 XX
 XX AC AD257693;
 XX
 XX DT 30-JUN-2005 (first entry)
 XX
 XX DE Anti-cMet antibody 13.3.2 heavy chain protein.
 XX
 XX antibody engineering; cytoskeletal; vulnery; vasotropic; cardiant;
 KW monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;
 KW gastrointestinal ulcer; ischemia; transplant rejection;
 KW myocardial infarction; reperfusion injury; resensitis; angioplasty;
 KW vascular disease; cancer; retinopathy; endometriosis; arthritis;
 KW Alzheimer's disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;
 KW antibody.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 1..19
 FT Peptide /note= "signal peptide"
 FT 14
 FT Misc-difference /note= "encoded by SCA"
 FT 20..462
 FT Protein /note= "mature antibody 13.3.2 heavy chain protein"
 FT 42
 FT Misc-difference /note= "encoded by RAG"
 FT 50..54
 FT Region /note= "complementarity determining region 1"

FT	Region	69..85
FT	/note= "complementarity determining region 2"	
FT	Misc-difference	97
FT	/note= "encoded by WCA"	
FT	Region	118..125
FT	/note= "complementarity determining region 3"	
XX		
XX	GB2404660-A.	
XX		
PD	09-FEB-2005.	
XX		
PF	04-AUG-2004; 2004GB-00017384.	
XX		
XX	04-AUG-2003; 2003US-0492432P.	
PR	(PEIZ) PEIZER PROD INC.	
PA	(ABGE-) ABGENIX INC.	
XX		
P1	Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL,	
PI	Jia X;	
XX		
DR	WPI, 2005-145169/16.	
XX	N-PSDB; ADZ57692.	
PT		
PT	Human monoclonal antibody or antigen-binding portion that specifically binds to c-Met, useful for treating cancer by inhibiting c-Met or for promoting tissue regeneration and wound healing by activating c-Met.	
XX		
PS	Claim 5; SEQ ID NO 2; 126pp; English.	
CC		
CC	The invention relates to a human monoclonal antibody (I) or its antigen-binding portion that specifically binds to c-Met, comprises a heavy chain having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is lysine and X4 is threonine, and a light chain having a fully defined sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both chains are without a signal sequence. All the sequences are fully defined in the specification. (I) is useful for the manufacture of a medicament for treating a hyperproliferative disorder in a subject, where the antibody or its portion is a c-Met antagonist. (I) is useful for manufacture of a medicament for promoting wound healing or tissue regeneration in a subject, where the antibody, antigen-binding portion or the composition activates c-Met. (I) which has a c-Met agonist activity is useful in tissue regeneration or wound healing (skin ulcers or gastric ulcers), or treating ischemia associated with kidney transplant rejection, for attenuating toxicity associated with cyclosporin treatment after transplant surgery, for treating myocardial infarction, cardiac ischemia due to reperfusion injury, restenosis after angioplasty or vascular diseases. (I) which has a c-Met antagonist activity is useful for treating cancers of brain, lung, squamous cell, bladder, neck, liver, prostate, etc., proliferative vitreoretinopathy, proliferative diabetic retinopathy, endometriosis, and arthritis, for inhibiting plaque formation in Alzheimer's disease, inhibiting cellular mitogenic responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas. (I) is useful for detecting c-Met in a biological sample in vitro or in vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has selectivity for c-Met that is at least 100 times greater than their selectivity for insulin like growth factor I receptor. This sequence corresponds to the antibody 13.3.2 heavy chain used in the invention.	
XX		
SQ	Sequence 462 AA;	
QY	Query Match	86.2%; Score 2146; DB 9; Length 462;
	Best Local Similarity	86.8%; Pred. No. 1,9e-121;
	Matches	401; Conservative 23; Mismatches 38; Indels 0; Gaps 0
DB		
	1 MECSCVMLFLSLGTAGVLSREVLDQSGPELVKPGASVKRSCAKSGYTGYTHIMNKQS	60
	: :	
	1 MDMTSTILFLVAATGACAHSDVQLVDSGAELKKPKGASVKVSKCASGGTFTSYGPSVRQAP	60
QY		
	61 GKSLSEMGITTYRNNGANGNOKFKGAATLTVDSSSTAYMELRTLTSEDSAVTYYCGKRSTW	120
	: :	
	61 OGGLSEMWGMIVASNSNGNTYAOKLQGVVMTTDTTSXAYMEIRLSINSDTAIVYCARVYA	120

Oy		121 DDPEDVMOGQITLTIVTSASRTKSGSVPRILAPCSRSTSESLAALGLCYMDYFPEPPTVMNSG	180
Dd		121 DYADVYGQGTLVTWTVSSASTKGPSVEPLAPCSRSSTESLTAALGLCYMDYFPEPPTVMNSG	180
Oy		181 ALTMSGHTPPALIOSSGLYSLSVVTPVPSSNFGOTYTCAVDHKPSNTKYDKTERKCVC	240
Dd		181 ALTMSGHTEPALIQQSGLXLSLVTTVPSSNFGRGTTCNVDDHKSPSTTKDIVERKCCV	240
Oy		241 ECPDCAPPVAGPSVFLEFPFKPKDTLMISRTPEVTCVVWDVSHPEDPVQFMNYDVGEVA	300
Dd		241 ECPCRCAPPVAVGPSVFLEFPFKPKDTLMISRPEVTCVVWDVSHPEDPVQFMNYDVGEVA	300
Oy		301 NATTKREBGFNSTRRVSYVLTVNHODMLNKKEYCKAKSNKGLPAPIEKTISTKKOPRE	360
Dd		301 NAAIKEREBGFNSTFRVSYVLTVNHQDLNLKEKCKVKSNKGLPAPIEKTIISKTKQPRES	360
Oy		361 PQYYTLPPSRHEMTKNQVSLCTLYGVFPSPDIAYEMBSNGOPENNYKITTPMLDSDGSFF	420
Dd		361 PQTYYLPFERBEKTNKVSLCTLVGFTFPSDIAYEMBSNQGPENNNYKITTFPMLDSDGSFF	420
Oy		421 LVSKLLTYDKSRMQOGNVFSCSVMEBALHNHYTGKSLSISPCK	462
Dd		421 LYSKLTYDKSRMQGGNVFSCSYMFBALHHNTYTGKSLSPCK	462
RESULT_8			
ID	ADTS1705	standard; protein; 446 AA.	
AC	ADTS1705;		
KX			
XX			
DT	13-JAN-2005	(first entry)	
XX			
DE	ViaElizunab antibody gamma-Zm3 heavy chain mutant M42BL.		
XX			
KM	Humanised; antibody; immunoglobulin G; IgG; gamma-Zm3 heavy chain;		
KM	FcRn binding affinity; serum half-life; dactilizumab; foncilizumab;		
KW	vializumab; M200; cancer; inflammatory disorder; asthma;		
KW	autoimmune disease; viral infection; cyclostatic; antiinflammatory;		
KX	antiaesthetic; immunosuppressive; virucide; mutant; mutein.		
OS	Homo sapiens.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Misc-difference 427	/note= "Substitution of wild-type Met to Leu"	
FN	WO2004092219-A2.		
PJ			
PD	28-OCT-2004.		
XX			
PF	09-APR-2004; 2004MC-US011213.		
XX			
PR	10-APR-2003; 2003US-0462014P.		
PR	03-JUN-2003; 2003US-0475762P.		
PR	29-AUG-2003; 2003US-049904BP.		
PR	15-OCT-2003; 2003US-0068711B.		
XA	(PROT-) PROTEIN DESIGN LABS INC.		
XI	Hinton PR, Teuruehta N, Tso JY, Vasequez M,		
XX	WPt; 2004-758341/74.		
DR			
XX			
PT	New modified antibodies of class Igg that have altered binding affinities		
PT	for Fcrn or altered serum half-lives, useful for diagnosing or treating		
EZ	for e.g. cancer, inflammation, autoimmune diseases or viral infections.		
XS	Claim 22; SEQ ID NO 138, 157pp; English.		
CC	The present invention relates to a modified human antibody of class		
CC	immunoglobulin G (IgG) where at least one amino acid residue from the		

QY 354 TKGQREPOVYTLPPSRREMTKNQVSLCTLVKGFYPSDIAMWESNGOPENNYKTTTPML 413
 DB 361 TKGQREPOVYTLPPSRREMTKNQVSLCTLVKGFYPSDIAMWESNGOPENNYKTTTPML 420
 QY 414 DSDGSFPLYSKLTVDKSRMVGQNVFSCSVMEHALHNHTYQKSLSPGK 462
 DB 421 DSDGSFPLYSKLTVDKSRMVGQNVFSCSVMEHALHNHTYQKSLSPGK 469
 RESULT 11
 ADTS1703 standard; protein; 446 AA.
 ADTS1703;
 ADTS1703; (first entry)
 13-JAN-2005
 Visilizumab antibody gamma-2M3 heavy chain mutant T250D.
 Humanised; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;
 FcRn binding affinity; serum half-life; dacilizumab; fontolizumab;
 visilizumab; M200; cancer; inflammatory disorder; asthma;
 autoimmune disease; viral infection; cytostatic; antiinflammatory;
 antiaesthetic; immunosuppressive; virucide; mutant; mutain.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers
 Misc-difference 249
 FT note= "Substitution of wild-type Thr to Asp"
 PM WO2004092219-A2.
 PD 28-OCT-2004.
 XX 09-APR-2004; 2004WO-US011213.
 PF 10-APR-2003; 2003US-0462014P.
 PR 03-JUN-2003; 2003US-0475762P.
 PR 29-AUG-2003; 2003US-0499048P.
 PR 15-OCT-2003; 2003US-00687118.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA Hinton PR, Teurushita N, Tso JY, Vasquez M;
 DR WPI: 2004-758341/74.
 XX
 PT New modified antibodies of class IgG that have altered binding affinities
 PT for FcRn or altered serum half-lives, useful for diagnosing or treating
 PT for e.g. cancer, inflammation, autoimmune diseases or viral infections.
 PS Claim 22; SEQ ID NO 136; 157bp; English.
 CC The present invention relates to a modified human antibody of class
 CC immunoglobulin G (IgG) where at least one amino acid residue from the
 CC heavy chain constant (CH) region selected from amino acid residues 250,
 CC 314 and 428 is different from that present in an unmodified class IgG
 CC antibody, and where the FcRn binding affinity and/or serum half-life of
 CC the modified antibody is altered relative to that of the unmodified
 CC antibody. The numbering of the residues in the heavy chain is that of the
 CC EU index. Also disclosed are methods of modifying an antibody of class
 CC IgG and producing the modified antibody cited, and a pharmaceutical
 CC composition comprising the above modified immunoglobulins, proteins and
 CC other bioactive molecules having altered half-lives. The unmodified or
 CC naturally occurring class IgG antibody is selected from dacilizumab,
 CC fontolizumab, visilizumab and M200. The amino acid residue 250 from the
 CC heavy chain constant region is glutamic acid or glutamine, or the amino
 CC acid residue 428 from the heavy chain constant region is phenylalanine or
 CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
 CC constant region is glutamic acid and the amino acid residue 428 from the

CC heavy chain constant region is phenylalanine, or the amino acid residue
 CC 250 from the heavy chain constant region is glutamine and the amino acid
 CC residue 428 from the heavy chain constant region is phenylalanine, or the
 CC amino acid residue 250 from the heavy chain constant region is glutamine
 CC and the amino acid residue 428 from the heavy chain constant region is
 CC leucine. The modified therapeutic antibody of class IgG has an in vivo
 CC elimination half-life of at least 1.3-fold longer than that of the
 CC corresponding unmodified class IgG antibody. The composition and methods
 CC of the invention are useful for various diagnostic and therapeutic
 CC purposes, especially in the treatment of cancer, inflammatory disorders
 CC (e.g. asthma), autoimmune diseases or viral infections. The present
 CC sequence represents a mutated region of a humanised antibody. Note: The
 CC position of the mutation is numbered according to the EU index.
 SO Sequence 446 AA;
 Query Match 86.0%; Score 2142.5; DB 8; Length 446;
 Best Local Similarity 89.7%; Pred. No. 2.9e-121;
 Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1;
 QY 20 EVOLQSGPELVKPKASVYKMSCKASGYGTYYIHMMQSHKSLIEWIYIPNNNGNGY 79
 DB 1 QVQLVQSGAEYKPKASVYKMSCKASGYFTITTHMWRQAPQGISMNGYINPRSGYTHY 60
 QY 80 NQKFKGKATLTVDKSSSTAYNELRTLTSBDSAIVYVYCGRSTWDDPD--YMGQGITLVYSS 136
 DB 61 NQKFKGKATLTVDKSSSTAYNELRTLTSBDSAIVYVYCGRSTWDDPD--YMGQGITLVYSS 120
 QY 137 ASTKPSVFPPLAPGCRSTSESTALGCLVKDYFPEPVVSNNGSLTSGVHTFPVAVLQSS 196
 DB 121 ASTKPSVFPPLAPGCRSTSESTALGCLVKDYFPEPVVSNNGSLTSGVHTFPVAVLQSS 180
 QY 197 GLYSLSVTVVTPSSVFGQYTCNDVHKPSMTKVDYERKCCVCPCPAPVAVGSPVYF 256
 DB 181 GLYSLSVTVVTPSSVFGQYTCNDVHKPSMTKVDYERKCCVCPCPAPVAVGSPVYF 240
 QY 257 LFPPEKDDLMISRPEVTCVVDVSHEDPEVQFMVYDGVENHAKTPRREQFNSTFR 316
 DB 241 LFPPEKDDLMISRPEVTCVVDVSHEDPEVQFMVYDGVENHAKTPRREQFNSTFR 300
 QY 317 VVSVLTVVHQMVLNKEKYCKVSNKGLPAPIEKTSKTKGQREPOVYTLPPSRREMTKN 376
 DB 301 VVSVLTVVHQMVLNKEKYCKVSNKGLPAPIEKTSKTKGQREPOVYTLPPSRREMTKN 360
 QY 377 QVSLCTLVKGFYPSDIAMWESNGOPENNYKTTTPMLDSDGSFPLYSKLTVDKSRMVGQNV 436
 DB 361 QVSLCTLVKGFYPSDIAMWESNGOPENNYKTTTPMLDSDGSFPLYSKLTVDKSRMVGQNV 420
 QY 437 VFSCSVMEHALHNHTYQKSLSPGK 462
 DB 421 VFSCSVMEHALHNHTYQKSLSPGK 446
 RESULT 12
 ADTS1704 standard; protein; 446 AA.
 ADTS1704;
 ADTS1704;
 13-JAN-2005 (first entry)
 Visilizumab antibody gamma-2M3 heavy chain mutant T250D.
 Humanised; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;
 FcRn binding affinity; serum half-life; dacilizumab; fontolizumab;
 visilizumab; M200; cancer; inflammatory disorder; asthma;
 autoimmune disease; viral infection; cytostatic; antiinflammatory;
 antiaesthetic; immunosuppressive; virucide; mutant; mutain.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers

FT	Misc-difference	249	
FT		/note=	"Substitution of wild-type Thr to Gln"
XX			
PN	WO2004092219-A2.		
XX			
PD	28-OCT-2004.		
XX			
PE	09-APR-2004;	2004WO-US011213.	
XX			
PR	10-APR-2003;	2003US-0462014P.	
PR	03-JUN-2003;	2003US-047562P.	
PR	29-AUG-2003;	2003US-0499048P.	
PR	15-OCT-2003;	2003US-0068711B.	
XX			
PA	(PROT-)	PROTEIN DESIGN LABS INC.	
XX			
PI	Hinton PR,	Teurushita N,	Tso JY, Vasquez M;
XX			
DR	WPI;	2004-758341/74.	
XX			
PT	New modified	antibodies of class Igg	that have altered binding affinities
PT	for Fc γ n	or altered serum half-lives,	useful for diagnosing or treating
PT	for e.g.	cancer, inflammation,	autoimmune diseases or viral infections.
XX			
PS	Claim 22;	SEQ ID NO 137;	157pp; English.

The present invention relates to a modified human antibody of class immunoglobulin G (IgG) where at least one amino acid residue from the heavy chain constant (CH) region selected from amino acid residues 250, 314 and 428 is different from that present in an unmodified class IgG antibody, and where the FcRn binding affinity and/or serum half-life of the modified antibody is altered relative to that of the unmodified antibody. The numbering of the residues in the heavy chain is that of the EU index. Also disclosed are methods of modifying an antibody of class IgG and producing the modified antibody cited, and a pharmaceutical composition comprising the above modified immunoglobulins, proteins and other bioactive molecules having altered half-lives. The unmodified or naturally occurring class IgG antibody is selected from dactinumb, fentolizumab, visilizumab and M200. The amino acid residue 250 from the heavy chain constant region is glutamic acid or glutamine, or the amino acid residue 428 from the heavy chain constant region is phenylalanine or leucine. Alternatively, the amino acid residue 250 from the heavy chain constant region is glutamic acid and the amino acid residue 428 from the heavy chain constant region is phenylalanine, or the amino acid residue 250 from the heavy chain constant region is glutamine and the amino acid residue 428 from the heavy chain constant region is phenylalanine, or the amino acid residue 250 from the heavy chain constant region is glutamine and the amino acid residue 428 from the heavy chain constant region is leucine. The modified therapeutic antibody of class IgG has an *in vivo* elimination half-life of at least 1.3-fold longer than that of the corresponding unmodified class IgG antibody. The composition and methods of the invention are useful for various diagnostic and therapeutic purposes, especially in the treatment of cancer, inflammatory disorders (e.g. asthma), autoimmune diseases or viral infections. The present invention represents a mutated region of a humanised antibody. Note: The position of the mutation is numbered according to the EU index.

[illegible]

Dd	121	ASTGPGSYFPLAPCSRSTSESTALAGCLVCKYFPEPVTYSNMSGALTSGVHTFPRAVLQSS	160
Qy	197	GLYSLSSTVVTVPSSNFGTQTYTCNVNDHKPSNTKVDKTVERRKCCVBCPCPAPVAGPSVF	256
Dd	181	GLYSLSSTVVTVPSSNFGTQTYTCNVNDHKPSNTKVDKTVERRKCCVBCPCPAPVAGPSVF	240
Qy	257	LPPPKDQTLMISTRPEVTCVVVDVSHDDPEYQFMWYVDGVVHNAKTKPRBEQFNSTR	316
Dd	241	LPPPKDQTLMISTRPEVTCVVVDVSHDDPEYQFMWYVDGVVHNAKTKPRBEQFNSTR	300
Qy	317	VSVVLTVVHOMLNKEYKCKVSNKGLPAPIEKTLSKTQGPDRPEQVYTLPPSRBEAMTN	376
Dd	301	VSVVLTVVHOMLNKEYKCKVSNKGLPAPIEKTLSKTQGPDRPEQVYTLPPSRBEAMTN	360
Qy	377	QVSLTCLVKGFPYPSDIAVWESNNGQPPENNYKTTTPMLDSDSGSEFLYSKLTVDKSRMQQGN	436
Dd	361	QVSLTCLVKGFPYPSDIAVWESNNGQPPENNYKTTTPMLDSDSGSEFLYSKLTVDKSRMQQGN	420
Qy	437	VFSGSVHMEBALHNHTOKSLISPSPK	462
Dd	421	VFSGSVHMEBALHNHTOKSLISPSPK	446
RESULT 13			
ADTS1692			
ID	ADTS1692	standard; protein; 442 AA.	
AC	ADTS1692;		
XX			
DT	13-JAN-2005	(first entry)	
DE			
XX			
XX			
KW	Humanized; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;		
KW	FcRn binding affinity; serum half-life; dactlizumab; fortoalizumab;		
KW	visfalinumb; M200; cancer; inflammatory disorder; asthma;		
KW	autoimmune disease; viral infection; cytostatic; antinflammatory;		
KW	antiasumatic; immunosuppressive; virucide; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference	245	
FT	/note= "Substitution of wild-type Thr to Gln"		
XX			
XX	WO2004092219-A2.		
PD	28-OCT-2004.		
XX			
PF	09-APR-2004; 2004MO-US011213.		
XX			
PR	10-APR-2003; 2003US-0462014P.		
PR	03-JUN-2003; 2003US-0475762P.		
PR	29-AUG-2003; 2003US-0495048P.		
PR	15-OCT-2003; 2003US-00687118.		
PA	(PROT-) PROTEIN DESIGN LABS INC.		
XX			
PI	Hinton PR, Tsurushita N, Tso JY, Vasquez M,		
XX			
DR	WPI; 2004-758341/74.		
XX			
PT	New modified antibodies of class IgG that have altered binding affinities		
PT	for FcRn or altered serum half-lives, useful for diagnosing or treating		
PT	for e.g. cancer, inflammation, autoimmune diseases or viral infections.		
XX			
PS	Claim 16; SEQ ID NO 125; 157bp; English.		
XX			
CC	The present invention relates to a modified human antibody of class		
CC	immunoglobulin G (IgG) where at least one amino acid residue from the		
CC	heavy chain constant (CH) region selected from amino acid residues 250,		
CC	314 and 428 is different from that present in an unmodified class IgG		

ID	AD751692	standard; protein; 442 AA.
XX		
AC	AD751692;	
XX		
DT	13-JAN-2005	(first entry)
XX		
DE	Daclizumab antibody gamma-2M3 heavy chain mutant T250Q.	
XX		
KM	Humanized; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;	
KM	Fc γ chain binding affinity; serum half-life; daclizumab; fontolizumab;	
KM	vislizumab; M200; cancer; inflammatory disorder; asthma;	
KM	autoimmune disease; viral infection; cytostatic; antiinflammatory;	
KM	antiaschmatic; immunosuppressive; virucide; mutant; mutein.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 245	
FT	/note= "Substitution of wild-type Thr to Gln"	
XX		
FN	WO2004092219-A2.	
XX		
PD	28-OCT-2004.	
XX		
PF	09-APR-2004; 2004WO-US011213.	
XX		
PR	10-APR-2003; 2003US-0462014P.	
PR	03-JUN-2003; 2003US-0475762P.	
PR	29-AUG-2003; 2003US-0499048P.	
PR	15-OCT-2003; 2003US-00687118.	
XX		
PA	(PROT-) PROTEIN DESIGN LABS INC.	
XX		
PI	Hinton PR, Tsurushita N, Tso JY, Vasquez M,	
XX		
DR	WPI; 2004-758341/74.	
XX		
PT	New modified antibodies of class IgG that have altered binding affinities	
PT	for Fc γ or altered serum half-lives, useful for diagnosing or treating	
PT	for e.g. cancer, inflammation, autoimmune diseases or viral infections.	
XX		
PS	Claim 16; SEQ ID NO 125; 157bp; English.	
XX		
CC	The present invention relates to a modified human antibody of class	
CC	immunoglobulin G (IgG) where at least one amino acid residue from the	
CC	heavy chain constant (CH) region selected from amino acid residues 250,	
CC	314 and 428 is different from that present in an unmodified class IgG	

ID	AD751692	standard; protein; 442 AA.
XX		
AC	AD751692;	
XX		
DT	13-JAN-2005	(first entry)
XX		
DE	Daclizumab antibody gamma-2M3 heavy chain mutant T250Q.	
XX		
KM	Humanized; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;	
KM	Fc γ chain binding affinity; serum half-life; daclizumab; fontcolizumab;	
KM	vislizumab; M200; cancer; inflammatory disorder; asthma;	
KM	autoimmune disease; viral infection; cytostatic; antinflammatory;	
KM	antiaschematic; immunosuppressive; virucide; mutant; mutein.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 245	
FT	/note= "Substitution of wild-type Thr to Gln"	
XX		
FN	WO2004092219-A2.	
XX		
PD	28-OCT-2004.	
XX		
PF	09-APR-2004; 2004MO-US011213.	
XX		
PR	10-APR-2003; 2003US-0462014P.	
PR	03-JUN-2003; 2003US-0475762P.	
PR	29-AUG-2003; 2003US-0499048P.	
PR	15-OCT-2003; 2003US-00687118.	
XX		
PA	(PROT-) PROTEIN DESIGN LABS INC.	
XX		
PI	Hinton PR, Tsurushita N, Tso JY, Vasquez M,	
XX		
DR	WPI; 2004-758341/74.	
XX		
PT	New modified antibodies of class IgG that have altered binding affinities	
PT	for Fc γ or altered serum half-lives, useful for diagnosing or treating	
PT	for e.g. cancer, inflammation, autoimmune diseases or viral infections.	
XX		
PS	Claim 16; SEQ ID NO 125; 157bp; English.	
XX		
CC	The present invention relates to a modified human antibody of class	
CC	immunoglobulin G (IgG) where at least one amino acid residue from the	
CC	heavy chain constant (CH) region selected from amino acid residues 250,	
CC	314 and 428 is different from that present in an unmodified class IgG	

[illegible]

Pt	Hinton PR,	Tanushita N,	Tso JY,	Vasquez M;
Xx				
Xx				
Dx	WPI; 2004-758341/74.			
Pr	New modified antibodies of class IgG that have altered binding affinities			
Pr	for Fc γ n or altered serum half-lives, useful for diagnosing or treating			
Pt	for e.g. cancer, inflammation, autoimmune diseases or viral infections.			
Xx				
Pt	Claim 22; SEQ ID NO 139; 157pp; English.			
Xx				
Xx	The present invention relates to a modified human antibody of class			
Cc	immunoglobulin G (IgG) where at least one amino acid residue from the			
Cc	heavy chain constant (CH) region selected from amino acid residues 250,			
Cc	314 and 428 is different from that present in an unmodified class IgG of			
Cc	antibody, and where the Fc γ n binding affinity and/or serum half-life of			
Cc	the modified antibody is altered relative to that of the unmodified			
Cc	antibody. The numbering of the residues in the heavy chain is that of the			
Cc	EU index. Also disclosed are methods of modifying an antibody of class			
Cc	IgG and producing the modified antibody cited, and a pharmaceutical			
Cc	composition comprising the above modified immunoglobulin, proteins and			
Cc	other bioactive molecules having altered half-lives. The unmodified or			
Cc	naturally occurring class IgG antibody is selected from dactilunab,			
Cc	fortilzunab, velsilzunab and M200. The amino acid residue 250 from the			
Cc	heavy chain constant region is glutamic acid or glutamine, or the amino			
Cc	acid residue 428 from the heavy chain constant region is phenylalanine or			
Cc	leucine. Alternatively, the amino acid residue 250 from the heavy chain			
Cc	constant region is glutamic acid and the amino acid residue 428 from the			
Cc	heavy chain constant region is phenylalanine, or the amino acid residue			
Cc	250 from the heavy chain constant region is glutamine and the amino acid			
Cc	residue 428 from the heavy chain constant region is phenylalanine, or the			
Cc	amino acid residue 250 from the heavy chain constant region is glutamine			
Cc	and the amino acid residue 428 from the heavy chain constant region is			
Cc	leucine. The modified therapeutic antibody of class IgG has an <i>in vivo</i>			
Cc	elimination half-life of at least 1.3-fold longer than that of the			
Cc	corresponding unmodified class IgG antibody. The composition and methods			
Cc	of the invention are useful for various diagnostic and therapeutic			
Cc	purposes, especially in the treatment of cancers, inflammatory disorders			
Cc	(e.g. asthma), autoimmune diseases or viral infections. The present			
Cc	sequence represents a mutated region of a humanised antibody. Note: The			
Cc	position of the mutation is numbered according to the EU index.			
Xx				
SQ	Sequence 446 AA:			
	Query Match	85.9%; Score 2139.5; DB 8; Length 446;		
	Beet Local Similarity	89.5%; Pred. No. 4.5e-121;		
	Matches 399; Conservative 17; Mismatches 27; Indels 3; Gaps 1			
Qy	20 EVOLQGSGPELVKPKASVKMSCKSAGTGYITIMQMOSHGKSLEWIGIYIPNNGXCY 79			
Dd	1 QVOLLVSQAELVKPKAPSVKSCAKSGYFIISTYMHWVAOPAQGLMMGIYNPRSGYTHY 60			
Qy	80 NOKFKGRKTLIVDSSSTAYMELRTLSRSDSAVVYVCGRSTWDMDPD---YMGQGTLLTVSS 136			
Dd	61 NOKLDRKATLLADNASASTAYHELSSLRSBDIAVYCARSAYIDYGFAVMGGITLVYSS 120			
Qy	137 ASTKGPSVFPLPACSRSTSSESTPAALGCCLVKKFYFPEPVTVSNNSGALTSGVHTPPAVLGSS 196			
Dd	121 ASTKGPSVFPLPACSRSTSSESTPAALGCCLVKKFYFPEPVTVSNNSGALTSGVHTPPAVLGSS 180			
Qy	197 GLYSLSISVTVPSSNFQTGYTTCNVDHKPSTNKDKTYERKCCVCEPCFPAPPAVGPSVF 256			
Dd	181 GLYSLSISVTVPSSNFQTGYTTCNVDHKPSTNKDKTYERKCCVCEPCFPAPPAVASVF 240			
Qy	257 LPPPKKDTLMISRPEVTCVVVDVSHDDPEYGFNMVYDVGEVNAHAKTRPREOFSNSTGR 316			
Dd	241 LPPPKKDTLMISRPEVTCVVVDVSHDDPEYGFNMVYDVGEVNAHAKTRPREOFSNSTGR 300			
Qy	317 VVSVLTVVHOHLNGKEKYCKSVNNGLPAPIEKTSKTGQRPREPOVYTLTPSPRESMTKN 376			
Dd	301 VVSVLTVVHOHLNGKEKYCKSVNNGLPAPIEKTSKTGQRPREPOVYTLTPSPRESMTKN 360			
Qy	377 QVSLTCLVKGFPSPDI AVEWESNQEPENNYKTTTPMLDSGSLFLYSKLITDKSKMQGN 436			

Db	361	QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPMLDSDGSFLYSKLTVDKSRWQGN	420
Qy	437	VFSCSVMEALHNHYTKSLSPGK	462
Db	421	VFSCSVLHEALHNHYTKSLSPGK	446

Search completed: January 24, 2006, 18:52:20
Job time : 155.339 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:57:25 / Search time 11.5279 Seconds
(without alignments)
208.348 Million cell updates/sec

Title: US-10-828-782a-16

Perfect score: 1232
Sequence: 1 MKLPRLVLMFWIPASSD.....EVTHQGLSSPVTKSFRNGEC 237

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications AA New:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/ECT_NEM_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037	84.2	239	US-11-086-289-12	Sequence 12, Appl
2	1029	83.5	239	US-11-139-499-6	Sequence 6, Appl
3	980.5	79.6	219	US-11-080-587-8	Sequence 8, Appl
4	951	77.2	238	US-11-158-505-1	Sequence 1, Appl
5	951	77.2	238	US-11-158-505-3	Sequence 3, Appl
6	951	77.2	238	US-11-158-505-25	Sequence 25, Appl
7	951	77.2	238	US-11-158-505-27	Sequence 27, Appl
8	941	76.4	238	US-11-158-505-9	Sequence 9, Appl
9	941	76.4	238	US-11-158-505-11	Sequence 11, Appl
10	941	76.4	238	US-11-158-505-17	Sequence 17, Appl
11	941	76.4	238	US-11-158-505-19	Sequence 19, Appl
12	941	76.4	238	US-11-158-505-74	Sequence 15, Appl
13	919	74.6	233	US-11-128-900-15	Sequence 67, Appl
14	919	74.6	233	US-11-128-900-67	Sequence 65, Appl
15	916	74.4	235	US-11-128-900-14	Sequence 69, Appl
16	916	74.4	235	US-11-128-900-65	Sequence 28, Appl
17	915.5	74.3	234	US-11-128-900-17	Sequence 29, Appl
18	915.5	74.3	234	US-11-128-900-69	Sequence 20, Appl
19	912	74.0	218	US-11-158-505-4	Sequence 12, Appl
20	912	74.0	218	US-11-158-505-28	Sequence 20, Appl
21	909.5	73.8	236	US-11-096-046-29	Sequence 12, Appl
22	904.5	73.4	236	US-11-086-289-20	Sequence 20, Appl
23	902	73.2	218	US-11-158-505-12	Sequence 8, Appl
24	902	73.2	218	US-11-158-505-20	Sequence 8, Appl
25	901.5	73.2	236	US-11-086-289-8	Sequence 8, Appl

26	898.5	72.9	236	US-11-144-248-48	Sequence 48, Appl
27	898.5	72.9	236	US-11-144-222-48	Sequence 48, Appl
28	898	72.9	235	US-11-086-289-16	Sequence 16, Appl
29	892	72.4	218	US-11-004-590-229	Sequence 229, App
30	890.5	72.3	236	US-11-144-248-52	Sequence 52, Appl
31	890.5	72.3	236	US-11-144-222-52	Sequence 4, Appl
32	888.5	72.1	236	US-11-086-289-4	Sequence 804, App
33	887.5	72.0	384	US-11-000-463-804	Sequence 805, App
34	887.5	72.0	384	US-11-000-463-805	Sequence 806, App
35	887.5	72.0	384	US-11-000-463-806	Sequence 807, App
36	887.5	72.0	384	US-11-000-463-807	Sequence 335, App
37	887	72.0	363	US-11-000-463-335	Sequence 71, Appl
38	882	71.6	214	US-11-128-900-71	Sequence 47, Appl
39	880	71.4	218	US-11-084-554-11	Sequence 47, Appl
40	878.5	71.3	236	US-11-144-248-47	Sequence 47, Appl
41	878.5	71.3	236	US-11-144-222-47	Sequence 129, App
42	878	71.3	214	US-11-102-621-129	Sequence 11, Appl
43	877	71.2	214	US-11-025-712-11	Sequence 51, Appl
44	876.5	71.1	236	US-11-144-248-51	Sequence 51, Appl
45	876.5	71.1	236	US-11-144-222-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1	US-11-086-289-12	Sequence 12, Application US/11086289
Publication No.	US2006002929A1	
GENERAL INFORMATION:		
APPLICANT:	KHARE, SANJAY D.	
TITLE OF INVENTION:	MONOCLONAL ANTIBODIES	
FILE REFERENCE:	06843.0094-00000	
CURRENT APPLICATION NUMBER:	US/11/086, 289	
CURRENT FILING DATE:	2005-03-23	
PRIOR APPLICATION NUMBER:	60/555,396	
PRIOR FILING DATE:	2004-03-23	
NUMBER OF SEQ ID NOS:	26	
SOFTWARE:	Patentin Ver. 3.3	
SEQ ID NO 12		
LENGTH:	239	
TYPE:	PRT	
ORGANISM:	Homo sapiens	
US-11-086-289-12		
Query Match	84.2%; Score 1037; DB 7; Length 239;	
Best Local Similarity	83.7%; Pred. No. 7.6e-63;	
Matches	200; Conservative 16; Mismatches 21; Indels 2; Gaps 2;	
QY	1 MKLPRLVLMFWIPASSDVLMTQTPLSPVSLGDQASISCRSSQITVHSGNTYLEW 59	
DB	1 MRLAQLGLMLWVPGSSGDIWMTQTPLSPVTLGQPASISCRSSQSLVHSDGNTYLSW 60	
QY	60 YLQKRGPSKLLIYKVSRRPFGSGSGTDFTLKISRVEAEDGIVYYCFOGTHAP 119	
DB	61 LQKRPQPLIYKFKRFGVDPDRSGSGAGDTFTLKISRVEAEDGVYICQATQIP 120	
QY	120 YTFGGTLEIR-TAAPSVEIFPPSDEQLKSGTAVVCLNNFYPRKAYQWKNALQ 178	
DB	121 LTFGGTVDIKRTVAAPSVEIFPPSDEQLKSGTAVVCLNNFYPRKAYQWKNALQ 180	
QY	179 SGNQSESTEDSKDSTYSLSTLTLSKADYBEKRVACEVTHQGLSSPVTKSFRNGEC 237	
DB	181 SGNQSESTEDSKDSTYSLSTLTLSKADYBEKRVACEVTHQGLSSPVTKSFRNGEC 239	
RESULT 2	US-11-139-499-6	
Sequence 6, Application US/11139499		
Publication No.	US20050260205A1	
GENERAL INFORMATION:		
APPLICANT:	ANDERSON, DARRELL R.	

```

/ APPLICANT: HANNA, NABIL
/ APPLICANT: BRAMS, PETER
/ APPLICANT: HEARD, CHERYL
/ TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
/ TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
/ TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
/ FILE REFERENCE: 37003-273681
/ CURRENT APPLICATION NUMBER: US/11/139,499
/ CURRENT FILING DATE: 2005-05-31
/ PRIOR APPLICATION NUMBER: US/09/576,424
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: PCT/US97/19906
/ PRIOR FILING DATE: 1997-10-29
/ PRIOR APPLICATION NUMBER: 08/746,361
/ PRIOR FILING DATE: 1996-11-08
/ PRIOR APPLICATION NUMBER: 08/487,550
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 239
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-139-499-6

```

```

Query Match      83.5%; Score 1029; DB 7; Length 239;
Best Local Similarity 83.3%; Pred. No. 2,6e-62;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

```

```

QY 1 MCLPRL-VLMFWIPASSDVLMTQTPSLPVSIGDQASISCRSSQTIHNSGNTYLEW 59
DB 1 MSLPQLGLLLCVFSGSEVMTQSPSLPTTPSPASISCRSSQSLKHSNGDTFLSW 60
QY 60 YQKQGPSPKLIYKYSNFGVDPDRFSGSGSDTFTLKISRVEADLVGYCCFGTHAP 119
DB 61 YQKQGPSPKLIYKYSNFGVDPDRFSGSGSDTFTLKISRVEADLVGYCCFGTHAP 120
QY 120 YTFGGGTGLEIK-TAAPSVPFIPPSDQKSGTASVCLNNFYPREAKVQKVDNALQ 178
DB 121 PFGGQTKVETKRYTAAPSVFIFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQ 180
QY 179 SGNQSESVTEQDSKSTYSLSTLTLSKADYERKHKVYACEVTHQGLSSPYTKSFNRGEC 237
DB 181 SGNQSESVTEQDSKSTYSLSTLTLSKADYERKHKVYACEVTHQGLSSPYTKSFNRGEC 239

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RESULT 3

```

US-11-080-587-8
/ Sequence 8, Application US/11080587
/ Publication No. US2006002942A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ TITLE OF INVENTION: Calicheamicin Conjugates
/ FILE REFERENCE: AM101462
/ CURRENT APPLICATION NUMBER: US/11/080,587
/ CURRENT FILING DATE: 2005-03-15
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 219
/ TYPE: PRT
/ ORGANISM: Human/murine chimera
US-11-080-587-8

```

```

Query Match      79.6%; Score 980.5; DB 7; Length 219;
Best Local Similarity 84.5%; Pred. No. 4e-59;
Matches 185; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

```

```

QY 20 DVIAMTQTPSLPVSIGDQASISCRSSQTIHNSGNTYLEWYQKQSPKLIYKYSNFG 79
DB 1 DVIAMTQTPSLPVSIGDQASISCRSSQTIHNSGNTYLEWYQKQSPKLIYKYSNFG 60
QY 80 SGVPRFSGSGSDTFTLKISRVEADLVGYCCFGTHAPYTFGGGTGLEI-KTAAPSV 138

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DB 61 SGVPRFSGSGSDTFTLKISRVEADLVGYCCFGTHAPYTFGGGTGLEI-KTAAPSV 120
QY 139 FIFPSDQKLSGTSASVCLNNFYPREAKVQKVDNALQSGNSQSESVTEQDSKSTYSL 198
DB 121 FIFPSDQKLSGTSASVCLNNFYPREAKVQKVDNALQSGNSQSESVTEQDSKSTYSL 180
QY 199 SSTLTLSKADYERKHKVYACEVTHQGLSSPYTKSFNRGEC 237
DB 181 SSTLTLSKADYERKHKVYACEVTHQGLSSPYTKSFNRGEC 219

```

RESULT 4

```

US-11-158-505-1
/ Sequence 1, Application US/11158505
/ Publication No. US2006002921A1
/ GENERAL INFORMATION:
/ APPLICANT: WINSOR-HINES, DAMN
/ APPLICANT: RAO, PATRICIA
/ APPLICANT: RINGLER, DOUGLAS J
/ APPLICANT: PONATH, PAUL
/ TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
/ TITLE OF INVENTION: INDUCTION IN PRIMATES
/ FILE REFERENCE: T1N-031
/ CURRENT APPLICATION NUMBER: US/11/158,505
/ CURRENT FILING DATE: 2005-06-21
/ PRIOR APPLICATION NUMBER: 60/582,181
/ PRIOR FILING DATE: 2004-06-22
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 1
/ LENGTH: 238
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ REAGENT:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
/ OTHER INFORMATION: antibody light chain construct
US-11-158-505-1

```

```

Query Match      77.2%; Score 951; DB 7; Length 238;
Best Local Similarity 78.2%; Pred. No. 3.9e-57;
Matches 183; Conservative 24; Mismatches 25; Indels 2; Gaps 2;

```

```

QY 5 VLLVLMFWIPASSDVLMTQTPSLPVSIGDQASISCRSSQTIHNSGNTYLEWYQK 64
DB 6 ILVAVLLMWPGSTGDIWVQSPDLSAVSLGRATINCKASQSDY-DGDSYMNWYQK 64
QY 65 QGSPKLIYKYSNFGVDPDRFSGSGSDTFTLKISRVEADLVGYCCFGTHAPYTFGG 124
DB 65 GQPKLIYKYSNLSGVPDRFSGSGSDTFTLTSLQAEVAVVYCCQSLQDPPTFGG 124
QY 125 GTKLEIK-TAAPSVPFIPPSDQKSGTASVCLNNFYPREAKVQKVDNALQSGNSQ 183
DB 125 GTKVEIKRYTAAPSVFIFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQSGNSQ 184
QY 184 ESVTEQDSKSTYSLSTLTLSKADYERKHKVYACEVTHQGLSSPYTKSFNRGEC 237
DB 185 ESVTEQDSKSTYSLSTLTLSKADYERKHKVYACEVTHQGLSSPYTKSFNRGEC 238

```

RESULT 5

```

US-11-158-505-3
/ Sequence 3, Application US/11158505
/ Publication No. US2006002921A1
/ GENERAL INFORMATION:
/ APPLICANT: WINSOR-HINES, DAMN
/ APPLICANT: RAO, PATRICIA
/ APPLICANT: RINGLER, DOUGLAS J
/ APPLICANT: PONATH, PAUL
/ TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
/ TITLE OF INVENTION: INDUCTION IN PRIMATES
/ FILE REFERENCE: T1N-031
/ CURRENT APPLICATION NUMBER: US/11/158,505

```

[illegible][illegible]

RESULT 8
 US-11-158-505-9
 , Sequence 9, Application US/11158505
 , Publication No. US20060002921A1
 , GENERAL INFORMATION:
 , APPLICANT: WINSOR-HINES, DAWN
 , APPLICANT: RAO, PATRICIA
 , APPLICANT: RINGLER, DOUGLAS J
 , APPLICANT: PONATH, PAUL
 , TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
 , TITLE OF INVENTION: INDUCTION IN PRIMATES
 , FILE REFERENCE: TLN-031
 , CURRENT APPLICATION NUMBER: US/11/158, 505
 , CURRENT FILING DATE: 2005-06-21
 , PRIOR APPLICATION NUMBER: 60/582, 181

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? PRIOR FILING DATE: 2004-06-22
? NUMBER OF SEQ ID NOS: 76
? SOFTWARE: PatentIn Ver. 3.3
? SEQ ID NO 9
? LENGTH: 238
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
? OTHER INFORMATION: antibody light chain construct
? JS-11-158-505-9

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Query Match	76.4%	Score 941	DB 7	Length 238
Best Local Similarity	77.8%	Pred. No. 1.8e-56		
Matches 182	Conservative 24	Mismatches 26	Indels 2	Gaps 2

[illegible]

RESULT 9

Sequence 11, Application US/11158505

```

: GENERAL INFORMATION:
: APPLICANT: MINSOR-HINES, DAWN
: APPLICANT: RAO, PATRICIA
: APPLICANT: RINGLER, DOUGLAS J
: APPLICANT: PONATH, PAUL
: TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
: TITLE OF INVENTION: INDUCTION IN PRIMATES
: FILE REFERENCE: T1N-031
: CURRENT APPLICATION NUMBER: US/11/158,505
: CURRENT FILING DATE: 2005-06-21
: PRIOR APPLICATION NUMBER: 60/582,181
: PRIOR FILING DATE: 2004-06-22
: NUMBER OF SEQ ID NOS: 76
: SOFTWARE: Patentin Ver. 3.3
: SEQ ID NO 11
:
: LENGTH: 238
:
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
: OTHER INFORMATION: antibody light chain construct
: US-11-158-505-11

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Query Match	76.4%;	Score 941;	DB 7;	Length 238;
Best Local Similarity	77.8%;	Pred. No. 1.8e-56;		
Matches 182;	Conservative 24;	Mismatches 26;	Indels 2;	Gaps 2

OY 5 VRLIVLFMTF PASSDVLMTQTPLSIPVSLGDDASTSCSSSGQTTHASNGNTLEMYLOKP 64
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 6 ILLMVLILMWPGSGTGDIVMTGSPDSLAVLSGERATINCKAQSVDY - DSDSYMMVTQQXP 64

OY 65 GQSKLLIYNKSRFSGVPRFSGSSGGDTFLAKIRVAEQLGYRYCPGTGHAPYTFGG 12
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 65 GQPKLIIITASNISSESVPRFSGSSGGDTFTLTISLDAAEVAAAYTCQOSLQDPPTFGG 12
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 125 GTKLEIK-TAAADSVLIFPPDSBQLSGTASVVCILNNFYPREAKVMKVNDALQSGNSQ 18:

Db 125 GTKEVEIKRTVAALSVIFPPSDDEQKSGSTASTVCLINNFYRANKVQMKVDNALQSNQ 18

QY 184 ESVTEDSDKSDSYSLSTLTLSKADYERKHKYACEVTHQGLSPVYSFNRGEC 237

Dd 185 ESTEDSDKSDSYSLSTLTLSKADYERKHKYACEVTHQGLSPVYSFNRGEC 238

RESULT 10
US-11-158

; Sequence 17, Application US/11158505
 ; Publication No. US20060002921A1
 CURRENT INFORMATION

```

1  APPLICANT: WINSOR-HINES, DAWN
2  APPLICANT: RAO, PATRICIA
3  APPLICANT: RINGLER, DOUGLAS J
4  APPLICANT: POMATH, PAUL
5  TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
6  TITLE OF INVENTION: INDUCTION IN PRIMATES
7  FILE REFERENCE: TLN-031
8  CURRENT APPLICATION NUMBER: US/11/158,505
9  CURRENT FILING DATE: 2005-06-21
10 PRIOR APPLICATION NUMBER: 60/582,181
11 PRIOR FILING DATE: 2004-06-22
12 NUMBER OF SEQ ID NOS: 76
13 SOFTWARE: PatentIn Ver. 3.3
14 SEQ ID NO: 17
15 LENGTH: 238
16 TYPE: PR1
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
20 OTHER INFORMATION: antibody light chain sequence
21 US-11-158-505-17

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Query Match	76.4%;	Score 941;	DB 7;	Length 238;
Best Local Similarity	77.8%;	Pred. No. 1.8e-56;		
Matches 182;	Conservative 24;	Mismatches 26;	Indels 2;	Gaps 2

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Oy 5 VRLVYLFMPFI PASSSVLVTOTPELSI PSLGQOABISGRSSQOTVHSGNKTFLSEMYLQKP 64
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Db 6 ILLMVLTLNPGSTGDI VMTQSPDSLANSLSGERATITNCKAASQSDY -DGSYTHMYQOKP 64

Oy 65 GQSPKLLIYKVSNRFSFGVPDRFSGSGSGDTFTLKI SRVEADLGVYCFQGTTHA PYTFQG 124
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Db 65 GQPPKLLIYVANSLSGEGVDRFSGSGSGDTFTLITSLQAEDVAHYVCQSLAQDPPTFGG 124

Oy 125 GTKLKLT-THAAPSVTI PPPSDQLKSGTASVYCLANNFPPEAKVQMKDVALQSGNSQ 184
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Db 125 GTVEYIKRTVAALSVFI PPPSDQLKSGTASVYCLANNFPPEAKVQMKDVALQSGNSQ 184

Oy 184 EASYTEDQSDQSYSLSSLTLSKADYBKHKYVACEVTHQGLSPPTYSFNNRGEC 237
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Db 185 EASYTEDQSDQSYSLSSLTLSKADYBKHKYVACEVTHQGLSPPTYSFNNRGEC 238

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US-11-158-

; Sequence 19, Application US/11158505
; Publication No. US20060002921A1

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? SEQ ID NO: 19
? LENGTH: 238
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
? OTHER INFORMATION: antibody light chain construct
?S-11-158-505-19

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Query Match	76.4%;	Score 941;	DB 7;	Length 238;
Best Local Similarity	77.8%;	Pred. No. 1.8e-56;		
Matches 182;	Conservative 24;	Mismatches 26;	Indels 2;	Gaps 2

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QY 5 VRLVLMFMFIPASSSVLMTOTPLSPVSLGQASISCRSSQTIYHSNGNTIEMYLQKP 64
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QY 65 GQSPKLLIYKVSNRFSGVDRFSGSGSGTFTLKISRVAEDLGVYCFQGTNAPYTFGG 124
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Db 65 GQPPKLLIYVASNLSGSDVDRFSGSGSGTFTLTISLQAEADVAVYCYQGSLOPPFFGG 124

QY 125 GTLTLEIK-TTAAASVYIIFPPSDGQLKSGTASIVCLINFFPREAKVQMKDNLAQSNQ 183
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QY 184 ESTVEODSKDSTVLSSTLTLSKADYEKKYVACEVTHQGLSSPTYSFNNGEC 237
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Db 185 ESTVEODSKDSTVLSSTLTLSKADYEKKYVACEVTHQGLSSPTYSFNNGEC 238

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RESULT 12
US-11-158

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1  ? Sequence 74, Application US/11158505
2  ? Publication No. US20060002921A1
3  GENERAL INFORMATION:
4  APPLICANT: WINSOR-HINES, DAWN
5  APPLICANT: RAO, PATRICIA
6  APPLICANT: RINGLER, DOUGLAS J
7  APPLICANT: PONATH, PAUL
8  TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4
9  TITLE OF INVENTION: INDUCTION IN PRIMATES
10 FILE REFERENCE: T1N-031
11 CURRENT APPLICATION NUMBER: US/11/158,505
12 CURRENT FILING DATE: 2005-06-21
13 PRIOR APPLICATION NUMBER: 60/582,181
14 PRIOR FILING DATE: 2004-06-22
15 NUMBER OF SEQ ID NOS: 76
16 SOFTWARE: Patentin Ver. 3.3
17 SEQ ID NO 74
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Dy 184 ESVTEQDSKDYSLSTLTISKADYEKKVAEVTTHGILSSPVYKSFNRGEC 237
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RESULT 13
US-11-128-900-15
; Sequence 15, Application US/11128900

```

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3
CURRENT APPLICATION NUMBER: US/11/128,900
PRIORITY FILING DATE: 2005-05-12
PRIORITY APPLICATION NUMBER: US 10/776649
PRIORITY FILING DATE: 2004-02-10
PRIORITY APPLICATION NUMBER: US 10/612497
PRIORITY APPLICATION NUMBER: 2003-07-01
PRIORITY APPLICATION NUMBER: US 09/472087
PRIORITY FILING DATE: 1999-12-23
PRIORITY APPLICATION NUMBER: US 60/113647
PRIORITY FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-15

```

Query Match	74.6%;	Score 919;	DB 7;	Length 233;
Best Local Similarity	74.1%;	Pred. No. 5.1e-55;		
Matches 177; Conservative	31;	Mismatches 23;	Indels 8;	Gaps 3

[illegible]

RESULT 14
US-11-128-900-67
Sequence 67, Application US/11128900
Publication No US2005028716A1
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVED, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOPFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3

```

; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-67
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```

Query Match 74.6%; Score 919; DB 7; Length 233;
Best Local Similarity 74.1%; Pred. No. 5.1e-55;
Matches 177; Conservative 31; Mismatches 23; Indels 8; Gaps 3;
```

```

QY 1 MCLPVRLI-VLMFWIPASSSDVLMQTPLSPVSLGDQASISCRSSQTIHNSNGNTYLEW 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 METPAQLFLFLMLPDTTGRIVLQSPGTSLSPGERATLSCRSQI-----SSYLAW 54

QY 60 YLQKPGQSPKLLIYKVSNRFGVPPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTAP 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 55 YQKPGQAPRLLIYGASRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGTSP 114

QY 120 YTFGGGTLEIK-TAAPSVFIFPPSDGQKSGTASVCLNNFYPREAKVQMKVDNALQ 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 115 YQKPGQAPRLLIYGASRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGTSP 174

QY 179 SGNQSESVTBQDSKQSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSPFNRGEC 237
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 SGNQSESVTBQDSKQSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSPFNRGEC 233
```

RESULT 15

```

US-11-128-900-14
; Sequence 14, Application US/11/128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-14
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```

Query Match 74.4%; Score 916; DB 7; Length 235;
Best Local Similarity 73.6%; Pred. No. 8.1e-55;
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```

Matches 176; Conservative 33; Mismatches 24; Indels 6; Gaps 3;

QY 1 MCLPVRLI-VLMFWIPASSSDVLMQTPLSPVSLGDQASISCRSSQTIHNSNGNTYLEW 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 METPAQLFLFLMLPDTTGRIVLQSPGTSLSPGERATLSCRSQI-----SSYLAW 56

QY 60 YLQKPGQSPKLLIYKVSNRFGVPPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTAP 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 YQKPGQAPRLLIYGASRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGTSP 116

QY 120 YTFGGGTLEIK-TAAPSVFIFPPSDGQKSGTASVCLNNFYPREAKVQMKVDNALQ 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 117 YTFGGGTLEIK-TAAPSVFIFPPSDGQKSGTASVCLNNFYPREAKVQMKVDNALQ 176

QY 179 SGNQSESVTBQDSKQSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSPFNRGEC 237
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 SGNQSESVTBQDSKQSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSPFNRGEC 235
```

```

Search completed: January 24, 2006, 19:13:53
Job time : 12.5279 secs
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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: January 24, 2006, 18:56:50 ; Search time 57.9785 Seconds
(without alignments)
1707.969 Million cell updates/sec

Title: US-10-828-782A-16
Perfect score: 1232
Sequence: 1 MKLPRLVLMFWIPASSD.....EVTHQGLSSPYTKSFNRGEC 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBSCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1232	100.0	237	5	US-10-828-782A-16
2	1164.5	94.5	238	5	US-10-497-475-19
3	1089.5	88.4	219	5	US-10-880-028-45
4	1089.5	88.4	219	5	US-10-880-320-45
5	1069.5	86.8	219	5	US-10-497-475-11
6	1049	85.1	239	6	US-11-031-485-36
7	1046	84.9	239	6	US-11-031-485-44
8	1043	84.7	239	6	US-11-031-485-68
9	1043	84.7	242	3	US-09-726-258-42
10	1039	84.3	239	4	US-10-292-088-32
11	1032	83.8	239	4	US-10-292-088-40
12	1030	83.6	220	4	US-10-737-208A-5
13	1030	83.6	220	6	US-11-040-071-2
14	1030	83.6	239	3	US-10-292-088-56
15	1029	83.5	239	3	US-09-758-173-6
16	1029	83.5	239	3	US-09-948-428B-6
17	1029	83.5	239	4	US-10-124-905-6
18	1029	83.5	239	4	US-10-124-807-6
19	1029	83.5	239	4	US-10-291-532-6
20	1029	83.5	239	4	US-10-428-408A-28
21	1029	83.5	239	4	US-10-428-894-28
22	1029	83.5	239	4	US-10-699-874-28
23	1029	83.5	239	5	US-10-986-780-6
24	1028.5	83.5	219	4	US-10-226-435A-11
25	1028.5	83.5	219	4	US-10-487-322-11
26	1028.5	83.5	219	5	US-10-487-326-11
27	1026.5	83.5	219	5	US-10-486-908-11

28	1028.5	83.5	219	5	US-10-512-527-11	Sequence 11, Appl
29	1028	83.4	239	4	US-10-292-088-16	Sequence 16, Appl
30	1025.5	83.2	238	6	US-11-031-485-40	Sequence 40, Appl
31	1025	83.2	247	4	US-10-466-164-69	Sequence 69, Appl
32	1024	83.1	239	6	US-11-131-648-21	Sequence 21, Appl
33	1024	83.1	239	6	US-11-131-648-51	Sequence 51, Appl
34	1023	83.0	239	4	US-10-292-088-102	Sequence 102, App
35	1022	83.0	239	4	US-10-292-088-8	Sequence 8, Appl
36	1021	82.9	239	6	US-11-031-485-66	Sequence 66, Appl
37	1020	82.8	239	4	US-10-404-724-39	Sequence 39, Appl
38	1020	82.8	239	4	US-10-292-088-64	Sequence 64, Appl
39	1020	82.8	239	4	US-10-292-088-80	Sequence 80, Appl
40	1020	82.8	239	5	US-10-816-276-35	Sequence 35, Appl
41	1019	82.7	239	4	US-10-404-724-12	Sequence 12, Appl
42	1019	82.7	239	4	US-10-404-724-47	Sequence 47, Appl
43	1019	82.7	239	5	US-10-816-276-8	Sequence 8, Appl
44	1019	82.7	239	5	US-10-816-276-43	Sequence 43, Appl
45	1019	82.7	239	6	US-11-031-485-32	Sequence 32, Appl

ALIGNMENTS

```

RESULT 1
US-10-828-782A-16
; Sequence 16, Application US/10828782A
; Publication No. US2004024268A1
; GENERAL INFORMATION:
; APPLICANT: Owens, S. Michael.
; TITLE OF INVENTION: Mouse/Human Chimeric Anti-Phencyclidine
; TITLE OF INVENTION: Antibody And Uses Thereof
; FILE REFERENCE: D6508
; CURRENT APPLICATION NUMBER: US/10/828,782A
; PRIOR APPLICATION NUMBER: 2004-04-21
; PRIOR FILING DATE: 2003-04-21
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 16
; LENGTH: 237
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of anti-PCP
; OTHER INFORMATION: ch-mab6B5 light chain.
US-10-828-782A-16

Query Match      100.0%; Score 1232; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKLPRLVLMFWIPASSDVLMTQPLSLPVSLDQASISCRSSQTIYHSNGNTYLEWY 60
DB      1 MKLPRLVLMFWIPASSDVLMTQPLSLPVSLDQASISCRSSQTIYHSNGNTYLEWY 60
QY      1 LKPKQSKLLIYKSNRFGVDFRFGSGGTDTLKI SRVEADLGVYCFQGHAPY 120
DB      1 LKPKQSKLLIYKSNRFGVDFRFGSGGTDTLKI SRVEADLGVYCFQGHAPY 120
QY      121 TFGGSKLEIKYAAPSVFIKPPSDQKSGTASVCLNNFYPREAKQWVDNALOSG 180
DB      121 TFGGSKLEIKYAAPSVFIKPPSDQKSGTASVCLNNFYPREAKQWVDNALOSG 180
QY      121 TFGGSKLEIKYAAPSVFIKPPSDQKSGTASVCLNNFYPREAKQWVDNALOSG 180
DB      121 TFGGSKLEIKYAAPSVFIKPPSDQKSGTASVCLNNFYPREAKQWVDNALOSG 180
QY      181 NSQESVTEQDSKDSYSLSTLTLSKADYERKRYVACEVTHQGLSSPYTKSFNRGEC 237
DB      181 NSQESVTEQDSKDSYSLSTLTLSKADYERKRYVACEVTHQGLSSPYTKSFNRGEC 237
RESULT 2
US-10-497-475-19
; Sequence 19, Application US/10497475
; Publication No. US20050142131A1
; GENERAL INFORMATION:

```



```
/ APPLICANT: Paul Robert Hinton
/ APPLICANT: Maximiliano J. Vaequez
/ TITLE OF INVENTION: Humanized Antibodies
/ FILE REFERENCE: X-14819
/ CURRENT APPLICATION NUMBER: US/10/497,475
/ CURRENT FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US 60/287,653
/ PRIOR FILING DATE: 2001-04-30
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 19
/ LENGTH: 238
/ TYPE: PRT
/ ORGANISM: humanized antibody
US-10-497-475-19

Query Match          94.5%; Score 1164.5; DB 5; Length 238;
Best Local Similarity 93.7%; Pred. No. 5.7e-55;
Matches 223; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 MRLPVRLVLMFWIPASSSDVMTQTPLSPVSLGDAISCRSSQTIIVHNGNTYLEWY 60
DB 1 MRLPVRLVLMFWIPASSSDVMTQSPSLPVLTLGGPAPISCRSSQNIHNSGNTYLEWY 60
QY 61 LQKPGQSPKLLIYKSNRRSGVPPDRPSGSGSDFTLTKISRVEADLGYYCCFGQTHAPY 120
DB 61 LQKPGQSPRLIYKSNRRSGVPPDRPSGSGSDFTLTKISRVEADLVGYCCFGQSHVPL 120
QY 121 TFGGGTKLEIK-TAAAPSVFIFFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQS 179
DB 121 TFGGGTKVTKITVAAPSVFIFFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQS 180
QY 180 GNSQSVTEQDSKDSSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 GNSQSVTEQDSKDSSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3
US-10-880-028-45
/ Sequence 45, Application US/10880028
/ Publication No. US20050163782A1
/ GENERAL INFORMATION:
/ APPLICANT: BRASLAWSKY, Gary R.
/ APPLICANT: GLASER, Scott
/ APPLICANT: YANG, Tzung-Hong
/ APPLICANT: HOPP, Jennifer
/ APPLICANT: CHINN, Paul
/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
/ TITLE OF INVENTION: OF BINDING POLYPEPTIDES
/ FILE REFERENCE: IDV-001
/ CURRENT APPLICATION NUMBER: US/10/880,028
/ CURRENT FILING DATE: 2004-06-28
/ PRIOR APPLICATION NUMBER: 60/483877
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/508810
/ PRIOR FILING DATE: 2003-10-03
/ PRIOR APPLICATION NUMBER: 60/515351
/ PRIOR FILING DATE: 2003-10-28
/ PRIOR APPLICATION NUMBER: 60/516030
/ PRIOR FILING DATE: 2003-10-30
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 219
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-880-028-45

Query Match          88.4%; Score 1089.5; DB 5; Length 219;
Best Local Similarity 95.9%; Pred. No. 5.3e-51;
Matches 210; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
```

```
QY 20 DVLMTQTPLSLPVSLGDAISCRSSQTIIVHNGNTYLEWYLOKPGQSPKLLIYVNSRF 79
DB 1 DFLMTQTPLSLPVSIGDQASISCRSSQSIIVHNGNTYLEWYLOKPGQSPKLLIYVNSRF 60
QY 80 SGVPPDRPSGSGSDFTLTKISRVEADLGYYCCFGQTHAPYTFGGGTLEIK-TAAAPSV 138
DB 61 SGVPPDRPSGSGSDFTLTKISRVEADLGYYCCFGQSHVPLTFGAGTKLEIKRTVAAPSV 120
QY 139 FIFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTSL 198
DB 121 FIFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTSL 180
QY 199 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 4
US-10-880-320-45
/ Sequence 45, Application US/10880320
/ Publication No. US20050163783A1
/ GENERAL INFORMATION:
/ APPLICANT: BRASLAWSKY, Gary R.
/ APPLICANT: GLASER, Scott
/ APPLICANT: YANG, Tzung-Hong
/ APPLICANT: HOPP, Jennifer
/ APPLICANT: CHINN, Paul
/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
/ TITLE OF INVENTION: OF BINDING POLYPEPTIDES
/ FILE REFERENCE: IDV-001
/ CURRENT APPLICATION NUMBER: US/10/880,320
/ CURRENT FILING DATE: 2004-06-28
/ PRIOR APPLICATION NUMBER: 60/483877
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/508810
/ PRIOR FILING DATE: 2003-10-03
/ PRIOR APPLICATION NUMBER: 60/515351
/ PRIOR FILING DATE: 2003-10-28
/ PRIOR APPLICATION NUMBER: 60/516030
/ PRIOR FILING DATE: 2003-10-30
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 219
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-880-320-45

Query Match          88.4%; Score 1089.5; DB 5; Length 219;
Best Local Similarity 95.9%; Pred. No. 5.3e-51;
Matches 210; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 20 DVLMTQTPLSLPVSLGDAISCRSSQTIIVHNGNTYLEWYLOKPGQSPKLLIYVNSRF 79
DB 1 DFLMTQTPLSLPVSIGDQASISCRSSQSIIVHNGNTYLEWYLOKPGQSPKLLIYVNSRF 60
QY 80 SGVPPDRPSGSGSDFTLTKISRVEADLGYYCCFGQTHAPYTFGGGTLEIK-TAAAPSV 138
DB 61 SGVPPDRPSGSGSDFTLTKISRVEADLGYYCCFGQSHVPLTFGAGTKLEIKRTVAAPSV 120
QY 139 FIFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTSL 198
DB 121 FIFPPSDQKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTSL 180
QY 199 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 5
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US-10-497-475-11
 ; Sequence 11, Application US/10497475
 ; Publication No. US20050142131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul Robert Hinton
 ; APPLICANT: Maximiliano J. Vasquez
 ; TITLE OF INVENTION: Humanized Antibodies
 ; FILE REFERENCE: X-14819
 ; CURRENT APPLICATION NUMBER: US/10/497,475
 ; CURRENT FILING DATE: 2004-06-01
 ; PRIOR APPLICATION NUMBER: US 60/287,653
 ; PRIOR FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 219
 ; TYPE: PRT
 ; ORGANISM: humanized antibody
 US-10-497-475-11

Query Match 86.8%; Score 1069.5; DB 5; Length 219;
 Best Local Similarity 93.2%; Pred. No. 6.2e-50;
 Matches 204; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 20 DVLMTQPLSLPVSIGDQASISCRSSQTIHNSNGTYLEWYLOKPGSPKLLIYKVSNR 79
 DB 1 DVMTQSPFLSLPVTIGQPASISCRSSQNIHNSNGTYLEWYLOKPGSPKLLIYKVSNR 60
 QY 80 SGVPRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAPYFGGTYLEIK-TAAAPSV 138
 DB 61 SGVPRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGSHPPLTFGGGTVEIKRTVAAPSV 120
 QY 139 FIFPPSDQQLSGTASVCLINNFYPRKAKVQWKDNLQSGNSQESTYEDSDKSTYSL 198
 DB 121 FIFPPSDQQLSGTASVCLINNFYPRKAKVQWKDNLQSGNSQESTYEDSDKSTYSL 180
 QY 199 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
 DB 181 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 6
 US-11-031-485-36
 ; Sequence 36, Application US/11031485
 ; Publication No. US20050232917A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PULLEN, NICHOLAS
 ; APPLICANT: MOLLOY, ELIZABETH
 ; APPLICANT: KELLERMANN, SIRID-AIMEE
 ; APPLICANT: GREEN, LARRY L.
 ; APPLICANT: HAAK-FRENSCH, MARY
 ; TITLE OF INVENTION: ANTIBODIES TO MADCAM
 ; FILE REFERENCE: ABX-PP6
 ; CURRENT APPLICATION NUMBER: US/11/031,485
 ; CURRENT FILING DATE: 2005-01-07
 ; PRIOR APPLICATION NUMBER: 60/535,490
 ; PRIOR FILING DATE: 2004-01-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 36
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-031-485-36

Query Match 85.1%; Score 1049; DB 6; Length 239;
 Best Local Similarity 84.1%; Pred. No. 8.3e-49;
 Matches 201; Conservative 19; Mismatches 17; Indels 2; Gaps 2;

QY 60 YLOKPGSPKLLIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 119
 DB 61 YLOKPGSPKLLIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 120
 QY 120 YTRGGTGLTEIK-TAAAPSVFIFPPSDQQLSGTASVCLINNFYPRKAKVQWKDNLQ 178
 DB 121 WTPGQGVTEIKRTVAAPSVFIFPPSDQQLSGTASVCLINNFYPRKAKVQWKDNLQ 180
 QY 179 SGNQSESTYEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
 DB 181 SGNQSESTYEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7
 US-11-031-485-68
 ; Sequence 68, Application US/11031485
 ; Publication No. US20050232917A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PULLEN, NICHOLAS
 ; APPLICANT: MOLLOY, ELIZABETH
 ; APPLICANT: KELLERMANN, SIRID-AIMEE
 ; APPLICANT: GREEN, LARRY L.
 ; APPLICANT: HAAK-FRENSCH, MARY
 ; TITLE OF INVENTION: ANTIBODIES TO MADCAM
 ; FILE REFERENCE: ABX-PP6
 ; CURRENT APPLICATION NUMBER: US/11/031,485
 ; CURRENT FILING DATE: 2005-01-07
 ; PRIOR APPLICATION NUMBER: 60/535,490
 ; PRIOR FILING DATE: 2004-01-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 68
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-031-485-68

Query Match 84.9%; Score 1046; DB 6; Length 239;
 Best Local Similarity 84.5%; Pred. No. 1.2e-48;
 Matches 202; Conservative 18; Mismatches 17; Indels 2; Gaps 2;

QY 1 MKLPTVRLI-VLMFWIPASSSDVLTMTQPLSLPVSIGDQASISCRSSQTIHNSNGTYLEW 59
 DB 1 MKLPTVRLI-VLMFWIPASSSDVLTMTQPLSLPVSIGDQASISCRSSQTIHNSNGTYLEW 60
 QY 60 YLOKPGSPKLLIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 119
 DB 61 YLOKPGSPKLLIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 120
 QY 120 YTRGGTGLTEIK-TAAAPSVFIFPPSDQQLSGTASVCLINNFYPRKAKVQWKDNLQ 178
 DB 121 WTPGQGVTEIKRTVAAPSVFIFPPSDQQLSGTASVCLINNFYPRKAKVQWKDNLQ 180
 QY 179 SGNQSESTYEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
 DB 181 SGNQSESTYEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
 US-11-031-485-44
 ; Sequence 44, Application US/11031485
 ; Publication No. US20050232917A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PULLEN, NICHOLAS
 ; APPLICANT: MOLLOY, ELIZABETH
 ; APPLICANT: KELLERMANN, SIRID-AIMEE
 ; APPLICANT: GREEN, LARRY L.
 ; APPLICANT: HAAK-FRENSCH, MARY
 ; TITLE OF INVENTION: ANTIBODIES TO MADCAM
 ; FILE REFERENCE: ABX-PP6
 ; CURRENT APPLICATION NUMBER: US/11/031,485
 ; CURRENT FILING DATE: 2005-01-07
 ; PRIOR APPLICATION NUMBER: 60/535,490

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; PRIOR FILING DATE 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 44
; LENGTH: 239
; TYPE: PRN
; ORGANISM: Homo sapiens
US-11-031-485-44

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Query Match	84.7%;	Score 1043;	DB 6;	Length 239;
Best Local Similarity	84.1%;	Pred. No. 1.7e-48;		
Matches 201; Conservative	19;	Mismatches 17;	Indels 2;	Gaps 2

Qy	1	MKLPVRLT-VLWMIIPASSDVLMTQTPSLPLVSLGDQASICRSQOTIVSNQNTYLEW	59
Qy	1	MRPLPQLSLGLMLMTIGSSADIVMTQTPSLSLVYTRQQPAISICSNQSLYSDGKTYLFW	60
Db	1	YLOKPGQSPDLLLYKVSNRPSGVPRFSGSGSGDTFTLKISRVEADLGVYVCFQGHAP	119
Qy	60	YLOKPGQSPDLLLYKVSNRPSGVPRFSGSGSGDTFTLKISRVEADLGVYVCFQGHAP	119
Db	61	YLOKPGQSPDLLLYKVSNRPSGVPRFSGSGSGDTFTLKISRVEADLGVYVCFQGHAP	120
Qy	120	YTFGGGTHLEIK-TAAAPSVYFIIPPSDEDLKSGTASVVCLLNNFYPREAKYQMKVDNALQ	178
Qy	121	MTFGQGGTKVEIKRTVAAPSVYFIIPPSDEDLKSGTASVVCLLNNFYPREAKYQMKVDNALQ	180
Db	121	MTFGQGGTKVEIKRTVAAPSVYFIIPPSDEDLKSGTASVVCLLNNFYPREAKYQMKVDNALQ	180
Qy	179	SGNSQESVLRBODSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSPYTKSNRREGC	237
Qy	181	SGNSQESVLRBODSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSPYTKSNRREGC	239
Db	181	SGNSQESVLRBODSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSPYTKSNRREGC	239

RESULT 9
US-09-726-258-42
; Sequence 42, Application US/09726258
; Publication No. US20030021790A1
; Publication Information

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; INFORMATION FOR SEQ ID NO: 42:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 242 amino acids
;       TYPE: Amino Acid
;       TOPOLOGY: Linear
US-09-726-258-42

```

Query Match	84.7%	Score 1043;	DB 3;	Length 242;
Best Local Similarity	86.4%	Pred. No. 1.7e-48;		
Matches 203; Conservative	12;	Mismatches 16;	Indels 4;	Gaps 2

```

Qy 7 LVLAMWIPASS---SDVLMTQTPPLSLVSLGDDQASISCRSSQCIYHNSNGTLYLEWLOK 63
Dy 8 LLASMWVBSIAINNAADIYMTQTPLSLVSLGDDQASISCRSSQSLVHGINTYLAHWLOK 67
Qy 64 PQGSPKLLIYKYNSRPSGVDRFSGSGSGCTDFTLKISRVEADLVGYIYCFQCHTAPYTFG 123
Dy 68 PQGSPKLLIYKYNSRPSGVDRFSGSGSGCTDFTLLRISVEARBDGLVFCQSSTHVPPLTFG 127
Qy 124 GGTKELEIKTA-AAPSYFIIPPSDBOLKSGTASVVCLLNFFPREAKQMKYDNLALOSGNS 182
Dy 128 AGTKELIKRAVNAFPTVFIIPPSBOLKSGTASVVCLLNFFPREAKQMKYDNLALOSGNS 187
Qy 183 QBSVTEBODKSDSYSLASSTLTLSKADYEHKRYVACEVTHQGLSSPYTKSFYRGEC 237
Dy 188 QBSVTEBODKSDSYSLASSTLTLSKADYEHKRYVACEVTHQGLSSPYTKSFYRGEC 242

```

RESULT 10
US-10-292-088-32
; Sequence 32, Application US/10292088
; Publication No. US20030211100A1
CENTRAL INTELLIGENCE AGENCY

1 GENERAL INFORMATION:
 2 APPLICANT: BEDIAN, VANE
 3 APPLICANT: GLADUE, RONALD P.
 4 APPLICANT: CORVALAN, JOSE
 5 APPLICANT: JIA, XIAO-CHI
 6 APPLICANT: FENG, XIAO
 7 TITLE OF INVENTION: ANTIBODIES TO CD40
 8 FILE REFERENCE: ABX-PF/3 US
 9 CURRENT APPLICATION NUMBER: 03/10/292,068
 10 CURRENT FILING DATE: 2003-03-14
 11 PRIOR APPLICATION NUMBER: 60/348,980
 12 PRIOR FILING DATE: 2001-11-09
 13 NUMBER OF SEQ ID NOS: 147
 14 SOFTWARE: PatentIn Ver. 2.1
 15 SEQ ID NO 32
 16 LENGTH: 239
 17 TYPE: PRT
 18 ORGANISM: Homo sapiens
 19 US-10-292-068-32

Query Match	84.3%	Score 1039;	DB 4;	Length 239;
Best Local Similarity	83.7%	Pred. No. 2.8e-48;		
Matches 200; Conservative	17;	Mismatches 20;	Indels 2;	Gaps 2

Qy	1	MDLPLVLT- VWEMWIPASSSDVIA MOTPLSLPEVSLGDA SISCSGQITVSNNTLEW	59
Qy	2	MDLPLVLT- VWEMWIPASSSDVIA MOTPLSLPEVSLGDA SISCSGQITVSNNTLEW	59
Db	1	MRPLPAQLGLMLM WSSGSDIVMTQSPSL PVTYGEPAASISCSG SOSGLHTHNGYTFDM	60
Qy	60	YLQKPGQSPFLTL YKYSNRPFSGVDP RFSGSGSGDTFTLK ISRVAEADLGVYTC QGHAP	119
Db	61	YLQKPGQSPFLTL YLGSNRNASGVPR FSSGSGDTFTLKIS RVAEADLGVYTCQ ALQTP	120
Qy	120	YTFGGGTGLKLR- TAAAPSVFI PPSDRQLKSGTNAV CCLNNFYPRKATQ MVDNALQ	178
Db	121	YSGGGTGLKLRKT VAPSVFI PPSDEQLKSGTNAV CCLNNFYPRKATQ MVDNALQ	180
Qy	179	SGNSQSSVLRKDS KSTSTSLTSLSKAD YKHKVAVCEVTHQGL SPVTKSNRRC	237
Db	181	SGNSQSSVLRKDS KSTSTSLTSLSKAD YKHKVAVCEVTHQGL SPVTKSNRRC	239

RESULT 11
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: PENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match 83.8%; Score 1032; DB 4; Length 239;
Best Local Similarity 83.3%; Pred. No. 6, 7e-48;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MCLPRL-VLMFWIPASSDVLMTOTPLSLPVLISGDQASISCRSSQTIHNSNGTYLW 59
DB 1 MRLPQLGLMLMLWVGSSGSDIVMTQSPSLPVTGPBPASISCRSSQSVLYSNGYVLDW 60
QY 60 YLQKQSGPKLLIYKVSNSRFGVPRFSGSGGCTPFTLKISVREABDLYVYCFPGCTAP 119
DB 61 YLQKQSGPKLLIYKVSNSRFGVPRFSGSGGCTPFTLKISVREABDLYVYCFPGCTAP 120
QY 120 YTFGGCTKLEIK-TAAPSVPFIFPPSDDEQLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
DB 121 FTFGCTKVIDIKRTVAASVFIFFPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQ 180
QY 179 SGNQSESVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SGNQSESVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12
US-10-737-208A-5
; Sequence 5, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 5
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin light chain
US-10-737-208A-5

Query Match 83.6%; Score 1030; DB 4; Length 220;
Best Local Similarity 90.9%; Pred. No. 8e-48;
Matches 200; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 20 DVLMTQTPLSLPVSLISGDQASISCRSSQTIHNSNGTYLWYLOKQSGPKLLIYKVSNSF 79

DB 1 DVLMTQTPLSLPVTPGEPBASISCRSSQSLVHRNGTYLHWYLOKQSGPKLLIHKVSNSF 60
QY 80 SGVPRFSGSGGSDTFTLKISVREABDLYVYCFPGCTA-PFTFGCTKLEIK-TAAPS 137
DB 61 SGVPRFSGSGGSDTFTLKISVREABDLYVYCFPGCTA-PFTFGCTKLEIKRTVAAPS 120
QY 138 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNQSSESVTEODSKDSTYS 197
DB 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNQSSESVTEODSKDSTYS 180
QY 198 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 13
US-11-040-071-2
; Sequence 2, Application US/11040071
; Publication No. US20050202021A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: Anti-Cancer Antibodies with Reduced Complement Fixation
; FILE REFERENCE: LEX-031
; CURRENT APPLICATION NUMBER: US/11/040,071
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 60/538,348
; PRIOR FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 2
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-040-071-2

Query Match 83.6%; Score 1030; DB 6; Length 220;
Best Local Similarity 90.9%; Pred. No. 8e-48; 10; Indels 2; Gaps 2;
Matches 200; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 20 DVLMTQTPLSLPVSLISGDQASISCRSSQTIHNSNGTYLWYLOKQSGPKLLIYKVSNSF 79
DB 1 DVLMTQTPLSLPVTPGEPBASISCRSSQSLVHRNGTYLHWYLOKQSGPKLLIHKVSNSF 60
QY 80 SGVPRFSGSGGSDTFTLKISVREABDLYVYCFPGCTA-PFTFGCTKLEIK-TAAPS 137
DB 61 SGVPRFSGSGGSDTFTLKISVREABDLYVYCFPGCTA-PFTFGCTKLEIKRTVAAPS 120
QY 138 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNQSSESVTEODSKDSTYS 197
DB 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNQSSESVTEODSKDSTYS 180
QY 198 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 14
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: PENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09

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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-56

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Query Match	83.6%;	Score 1030;	DB 4;	Length 239;
Best Local Similarity	83.7%;	Pred. No. 8.5e-48;		
Matches 200;	Conservative 16;	Mismatches 21;	Indels 2;	Gaps 2

[illegible]

RESULT 15

US-09-758-173-6
; Sequence 6, Application US/09758173
; Publication No. US20010024648A1
; GENERAL INFORMATION:

1 APPLICANT: Anderson, Darrell R.
2 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
3 TO HUMAN B7.1 AND/OR B7.2 PRIMATED FORMS THEREOF."
4 TITLE OF INVENTION:
5 PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
6 IMMUNOSUPPRESSANTS"
7 NUMBER OF SEQUENCES: 12
8
9 CORRESPONDENCE ADDRESS: 12

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,316
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

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; INFORMATION FOR SEQ ID NO: 6
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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MOLECULE TYPE: protein;
US-09-758-173-6

Query Match	83.5%;	Score 1029;	DB 3;	Length 239;
Best Local Similarity	83.3%;	Pred. No. 9.6e-48;		
Matches 199;	Conservative 19;	Mismatches 19;	Indels 2;	Gaps 2;

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Oy 1 KKLPRLL-VMFMFPASSSVLMQTPSLSPVSLGADQASISCRSSQTVHANGMYLSM 59
    | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MSLPRQLIGLLLCVPSGSSGEVMTQSPSLPITGGERPASICRSGSLKSHNGDTFLSM 60

Oy 60 YLQKPGQSKLLIYKVSNRFGQVDFRFGSGSGSDTDFLLKISVEABDLGVYCFQGTAAIP 119
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Db 61 YQKRGQGPRLIIVKYSNRDSGVPRFRGSGGAGTDFLLKISAVEABDVGVYFCQGTATTP 120

Oy 120 YTFGGGTLEIK-THAAPSVPFRPSSDQLKSGTASVYCLNNFVPRKQVMKYNALQ 178
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 PTFGGGTVEIKRTVAAPSVPFRPSSDQLKSGTASVYCLNNFVPRKQVMKYNALQ 180

Oy 179 SGNSESVTEBODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGISLSPVTKSPNREGC 237
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Db 181 SGNSESVTEBODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGISLSPVTKSPNREGC 239

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Search completed: January 24, 2006, 19:13:07
Job time : 58.9785 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 24, 2006, 18:44:45 / Search time 77.3047 Seconds
(without alignments)

2163.001 Million cell updates/sec

Title: US-10-828-782A-16

Perfect score: 1232

Sequence: 1 MKLTVRLVLMFWIPASSSD.....EVTHQGLSSPYTKSPNNGEC 237

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060	86.0	239	2	Q8TCD0_HUMAN
2	1045	84.8	239	2	Q6P491_HUMAN
3	1032	83.8	239	2	Q8NEK0_HUMAN
4	1021.5	82.9	240	2	Q6PIH6_HUMAN
5	920.5	74.7	236	2	Q6PIH6_HUMAN
6	911	73.9	235	2	Q6GMV9_HUMAN
7	907.5	73.7	236	2	Q6PS58_HUMAN
8	901.5	73.2	236	2	Q6GMX8_HUMAN
9	900	73.1	235	2	Q6P491_HUMAN
10	896.5	72.8	236	2	Q6GMX1_HUMAN
11	894.5	72.6	236	2	Q6GMX0_HUMAN
12	893.5	72.5	236	2	Q6PIH7_HUMAN
13	892	72.4	235	2	Q6GMX0_HUMAN
14	884.5	71.8	234	2	Q72473_HUMAN
15	875.5	71.1	236	2	Q502W4_HUMAN
16	865.5	70.6	234	2	Q5EF66_HUMAN
17	865.5	70.3	236	2	Q6PIH4_HUMAN
18	864.5	70.2	236	2	Q6PIH7_HUMAN
19	860.5	69.8	236	2	Q6GMX9_HUMAN
20	859.5	69.8	236	2	Q723Y4_HUMAN
21	854.5	69.4	219	2	Q6S2C0_MOUSE
22	853.5	69.3	234	2	Q56919_HUMAN
23	821.5	66.7	239	2	Q58E08_MOUSE
24	798.5	64.8	234	2	Q5XKQ4_MOUSE
25	734	59.6	240	2	Q52L64_MOUSE
26	725	58.8	238	2	Q6C1S7_MOUSE
27	711.5	57.8	236	2	Q7TS98_MOUSE
28	692.5	56.2	234	2	Q4KM66_RAT
29	685.5	55.6	236	2	Q52L95_MOUSE
30	682	55.4	238	2	Q58E04_MOUSE
31	677.5	55.0	234	2	Q5M838_RAT

32	668	54.2	241	2	Q632X4_MOUSE
33	640.5	52.0	237	2	Q569Y8_MOUSE
34	629.5	51.1	235	2	Q5XFX8_MOUSE
35	623.5	50.5	235	2	Q58E06_MOUSE
36	619.5	50.3	189	2	Q56917_HUMAN
37	576.5	46.8	120	2	Q6P5R3_HUMAN
38	565	45.9	248	2	Q65207_MOUSE
39	551.5	44.8	243	2	Q6NTU5_XENTLA
40	545	44.2	237	2	Q7S236_XENTLA
41	544	44.2	106	1	KAC_HUMAN
42	541.5	44.0	239	2	Q5HZC6_XENTR
43	540.5	43.9	115	2	Q5F210_MOUSE
44	532	43.2	113	1	KV2G_MOUSE
45	529.5	43.0	133	1	KV2F_HUMAN

ALIGNMENTS

RESULT 1
Q8TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Scheffer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Strausberg R.;
DT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
RT nephritis-associated idiotype";
RT Nucleic Acids Res. 20:2601-0(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1551402;
RA Lauener-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiede R., Zocher I., Zachau H.G.;

RT "The human immunoglobulin kappa locus. Characterization of the
 RT duplicated A regions.";
 RL Eur. J. Immunol. 22:1023-1029 (1992).
 RN (5)
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8258341;
 RA Klein R., Jaenichen R., Zachau H.G.;
 RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
 RL Eur. J. Immunol. 23:3248-3262 (1993).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation.";
 RL Eur. J. Immunol. 23:391-397 (1993).
 DR EMBL, BC023362; AAH23362.1; -, mRNA.
 DR PIR, S32658; S32658.
 DR PIR, S34095; S34095.
 DR PIR, S40324; S40324.
 DR PIR, S40374; S40374.
 DR PIR, S42267; S42267.
 DR PIR, S42268; S42268.
 DR HSSP, P01834; 117Z.
 DR SMR, Q8TCD0; 21-237.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-sect; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS50290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 239 AA; 26235 MW; FACBDCAJ3803871D CRC64;

Query Match 86.0%; Score 1060; DB 2; Length 239;
 Best Local Similarity 85.4%; Pred. No. 2,9e-80;
 Matches 204; Conservative 18; Mismatches 15; Indels 2; Gaps 2;

QY 1 MCLPVRLL-VLMFMIPASSDYLMTQTPLSLVISGDOASISCRSSQTIHNSGNTYLEM 59
 DB 1 MCLPVRLL-VLMFMIPASSDYLMTQTPLSLVISGDOASISCRSSQTIHNSGNTYLEM 60
 QY 60 YLQKQSGSPKLIYKVSNRFSVGPDRFSGSGSGDTFTLKISVREADLGVVYCFQGTAP 119
 DB 61 FQQRGQSPRLIYKVSNRFSVGPDRFSGSGSGDTFTLKISVREADGVYFCMQGTMP 120
 QY 120 YTFGGGTKEIK-TPAAPSVPFIPPSPDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 178
 DB 121 STFGQGTKEIKRTVAAPSVFIFPPSDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 180
 QY 179 SGNSESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHQGLSPVTSFNRGEC 237
 DB 181 SGNSESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHQGLSPVTSFNRGEC 239

RESULT 2
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 ID Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
 AC Q6P491;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 OS Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE-Skin;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshlyuk S., Carinich P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalske U., Smallus D.B.,
 RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC063599; AAH63599.1; -, mRNA.
 DR HSSP, P01837; 1KCU.
 DR SMR, Q6P491; 21-237.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-sect; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS50290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDPFD35883 CRC64;

Query Match 84.8%; Score 1045; DB 2; Length 239;
 Best Local Similarity 83.7%; Pred. No. 5.3e-79;
 Matches 200; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

QY 1 MCLPVRLL-VLMFMIPASSDYLMTQTPLSLVISGDOASISCRSSQTIHNSGNTYLEM 59
 DB 1 MCLPVRLL-VLMFMIPASSDYLMTQTPLSLVISGDOASISCRSSQTIHNSGNTYLEM 60
 QY 60 YLQKQSGSPKLIYKVSNRFSVGPDRFSGSGSGDTFTLKISVREADLGVVYCFQGTAP 119
 DB 61 LHQRPQSPRLIYKVSNRFSVGPDRFSGSGSGDTFTLKISVREADGVYFCMQVSHFP 120
 QY 120 YTFGGGTKEIK-TPAAPSVPFIPPSPDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 178
 DB 121 RTFGQGTVEIKRTVAAPSVFIFPPSDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 180
 QY 179 SGNSESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHQGLSPVTSFNRGEC 237
 DB 181 SGNSESVTEODSKDSTYSLSTLTLSKADYERKHYACEVTHQGLSPVTSFNRGEC 239

RESULT 3
 Q8N8KO_HUMAN PRELIMINARY; PRT; 239 AA.
 ID Q8N8KO_HUMAN PRELIMINARY; PRT; 239 AA.
 AC Q8N8KO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 OS IGV1-5 protein.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

GN Name=IGKV1-5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Prostate;
 RA Director MGC Project;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1601042;
 RA Huber C., Kloebeck H.G., Zachau H.G.;
 RT "Ongoing V kappa-J kappa recombination after formation of a productive
 RT V kappa-J kappa coding joint.";
 RL Eur. J. Immunol. 22:1561-1565 (1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation.";
 RL Eur. J. Immunol. 23:391-397 (1993).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8258341;
 RA Klein R., Jaenichen R., Zachau H.G.;
 RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
 RL Eur. J. Immunol. 23:3248-3262 (1993).
 DR EMBL: BC030814; AAH30814.1; -, mRNA.
 DR PIR: S23638; S23638.
 DR PIR: S34091; S34091.
 DR PIR: S40342; S40342.
 DR PIR: S40357; S40357.
 DR HSSP: P01834; 117Z.
 DR SMR: Q8N8K0; 21-237.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF07654; C1-sect; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKOWN_1.
 DR Immunoglobulin domain.
 KW SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 83.8%; Score 1032; DB 2; Length 239;
 Best Local Similarity 82.8%; Pred. No. 6-4e-78;
 Matches 198; Conservative 19; Mismatches 20; Indels 2; Gaps 2;
 QY 1 MCLPVRLI-VIMFVPIPASSDVLMTQPLSLIPVSLIGDQASISCRSSQITVHSNGNTYLEW 59
 DB 1 MRLPQGLGLMLWVSGSSGDIWMTQSPISFPTFPGEPASISCRSSQGLHSDGYNVLDW 60
 QY 60 YLQKPGQSPKLLIYKVSIRPGVDPRFSGSGSDFTLKIRVEAEDEGVYVCFPGGTAP 119
 DB 61 YLQKPGQSPOLLILYGSRRASGVDPFRSGSGSDFTLKIRVEAEDEGVYVCFPGGTAP 120
 QY 120 YTPGGGTGLERK-TAAPSVEFIPPSDQLKSGTAVVCLINNFYPRBAKYQMKVDNALQ 178
 DB 121 QTFGGGTVEIKRITVAASVETFPSPDQLKSGTASVCLINNFYPRBAKYQMKVDNTLQ 180
 QY 179 SGNQSESVTEQDSKDSYSLSTLTLSKADYERKRVACEVTHQGLSSPVTKSFNRGEC 237
 DB 181 SGNQSESVTEQDSKDSYSLSTLTLSKADYERKRVACEVTHQGLSSPVTKSFNRGEC 239
 RESULT 4
 ID G6PIH6 HUMAN PRELIMINARY; PRT; 240 AA.
 AC G6PIH6;
 DT 05-JUN-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE IGKV1-5 protein.
 GN Name=IGKV1-5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Director MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC034142; AAH34142.1; -, mRNA.
 DR HSSP: P01837; 1KB5.
 DR SMR: G6PIH6; 23-240.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.

QY 179 SGNQSEVTEBDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGRG 237
 DB 178 SGNQSEVTEBDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGRG 236

RESULT 12
 O6P1H7 HUMAN PRELIMINARY; PRT; 236 AA.
 ID O6P1H7
 AC O6P1H7
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo
 NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034141; AAH34141.1; -; mRNA.
 DR HSSP; P01607; IAR2.
 DR SMR; P01607; IAR2.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003066; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25603 MW; 8BCE61106861213F CRC64;

Query Match 72.5%; Score 893.5; DB 2; Length 236;
 Best Local Similarity 73.2%; Pred. No. 2,3e-66;
 Matches 175; Conservative 24; Mismatches 33; Indels 7; Gaps 3;

QY 1 MCLPVRLT-VLWFWIPASSDVLMTQTPSLPLVLDQASISCRSQTIVHSGNTYLEM 59
 DB 3 MCVPSQLGLLMLPLGACDIDLTOSPSFSLASVDRVYITTCRASQGI-----SSYLLAM 57

QY 60 YLQKQSPKLLIYVNSRFGVDPDRFGSGSGDFTLKISRVNEDLCVYICFQHTAP 119
 DB 58 YQKPKAPNLLIYVNSRFGVDPDRFGSGSGDFTLTISRLQPEDPATYCCQQLNSP 117

QY 120 YTPGGGTLEIK-TAAPSVPFIFPPSDQLKSGTASVVCCLANNFYPREAKVOMKDNALQ 178
 DB 118 PTFGGGTVEIKRTYAAPSVPIFPSPDQLKSGTASVVCCLANNFYPREAKVOMKDNALQ 177

QY 179 SGNQSEVTEBDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGRG 237
 DB 178 SGNQSEVTEBDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGRG 236

RESULT 13
 O6GMNO HUMAN PRELIMINARY; PRT; 235 AA.
 ID O6GMNO
 AC O6GMNO
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE IGKV1-5 protein.
 GN Name=IGKV1-5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo
 NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG Director MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073792; AAH73792.1; -; mRNA.
 DR SMR; O6GMNO; 21-233.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003066; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 72.4%; Score 892; DB 2; Length 235;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:45:30 ; Search time 32.3863 Seconds

(without alignments)
1372.562 Million cell updates/sec

Title: US-10-828-782A-18

Perfect score: 2490

Sequence: 1 MECSCVMFLSLGTAGVLSF.....MREALHNRVTQKSLSPGK 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80.*

2: PIR1.*

3: PIR2.*

4: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1755	70.5	326	1 G2HU	Ig gamma-2 chain C
2	1605.5	64.5	327	1 G4HU	Ig gamma-4 chain C
3	1604	64.4	330	1 G4HU	Ig gamma-1 chain C
4	1599.5	63.2	469	2 S37483	Ig gamma-2a chain C
5	1578.5	63.4	377	2 A23511	Ig gamma-3 chain C
6	1569.5	63.0	377	2 A60764	Ig gamma-3 chain C
7	1549	62.2	446	2 S40295	Ig gamma-2a chain C
8	1545	62.0	474	1 G2MS11	Ig gamma-2b chain C
9	1490.5	59.9	475	2 S01321	Ig gamma-2b chain C
10	1481	59.5	470	2 S20800	Ig heavy chain pre
11	1465	58.8	472	2 S31459	Ig gamma-1 chain-
12	1430.5	57.4	444	2 PC4436	monoclonal antiod
13	1316	52.9	374	2 S69339	Ig heavy chain V r
14	1271	51.0	328	2 I47159	Ig gamma-2a chain
15	1265	50.8	328	2 I47160	Ig gamma-2b chain
16	1246	50.0	328	2 I47161	Ig gamma-2b chain
17	1236	49.6	328	2 I47160	Ig gamma-2b chain
18	1207.5	48.5	323	1 G4HB	Ig gamma-1 chain C
19	1176.5	47.2	329	1 G2GP	Ig gamma-1 chain C
20	1164	46.7	326	2 PS0017	Ig gamma-2 chain C
21	1151	46.2	255	4 S31866	Ig gamma-1 chain C
22	1145.5	46.0	308	2 C30554	Ig heavy chain C r
23	1143	45.9	324	1 G1MS	Ig gamma-1 chain C
24	1138	45.7	393	1 G1MS	Ig gamma-1 chain C
25	1134	45.5	234	1 G1MS	Ig gamma-1 chain C
26	1120.5	45.0	333	2 PS0018	Ig gamma-2b chain
27	1120	45.0	322	2 PS0019	Ig gamma-2a chain
28	1115.5	44.8	327	2 S06611	Ig gamma-2 chain C
29	1114	44.7	289	1 G3HWT	Ig gamma-3 heavy c

30	1111.5	44.6	329	2 S00847	Ig gamma-2c chain
31	1097	44.1	329	1 G3MSC	Ig gamma-3 chain C
32	1095	44.0	330	1 G2MSA	Ig gamma-2a chain
33	1090	43.8	399	1 G3MSM	Ig gamma-2a chain
34	1086	43.6	398	1 G3MSM	Ig gamma-3 chain C
35	1083.5	43.5	335	1 G2MSAB	Ig gamma-2a chain
36	1068	42.9	277	2 I47162	Ig gamma-4 chain C
37	1054	42.3	405	1 G2MSBM	Ig gamma-2b chain
38	943	37.9	548	2 S38864	Ig epsilon chain C
39	937.5	37.7	241	2 S69131	Ig heavy chain (DO
40	892.5	35.8	549	2 S04845	Ig heavy chain pre
41	857	34.4	246	2 S38950	Ig gamma chain - m
42	829	33.3	627	2 S14683	Ig mu chain precu
43	758.5	30.5	572	2 B46529	Ig y heavy chain (
44	725	29.1	220	2 A49444	Ig gamma-1 heavy c
45	721.5	29.0	249	2 S69340	Ig heavy chain VH1

ALIGNMENTS

RESULT 1

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain cor
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <RLL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BPC; GB:V00554; GB:J00230; NID:932
A>Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Accession: A92809
A:Contents: myeloma protein T11
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Cross-references: UNIPARC:UPI0000173791
R:Comell, G.B.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A>Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:8001357; PMID:1113060
A:Accession: A90752
A:Contents: myeloma protein Z1e
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Z1e
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidacti
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971

A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:7203500; PMID:4904472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:6906424; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger multimers.
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,146-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	70.5%;	Score 1755;	DB 1;	Length 326;
Best Local Similarity	100.0%;	Pred. No. 1.9e-94;		
Matches 326;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	13	ASTKGSVFPEFLACSSRSTSESTALGCVKVDYFPPPTVSNMNGLTGVTFFPAVLQSS	196
Db	1	ASTKGSVFPEFLACSSRSTSESTALGCVKVDYFPPPTVSNMNGLTGVTFFPAVLQSS	60
Qy	197	GLYLSSTVTVBPSNSNGTQTYTCNDHKSNTKVDKTYERKCYACRCPAPAPAGSVF	256
Db	61	GLYLSSTVTVBPSNSNGTQTYTCNDHKSNTKVDKTYERKCYACRCPAPAPAGSVF	120
Qy	257	LFPKPKDITLMSRTEPEVTCVVVDVSHEDPEVQFAMVYDGYEVNNAKTKPREQFNSIFR	316
Db	121	LFPKPKDITLMSRTEPEVTCVVVDVSHEDPEVQFAMVYDGYEVNNAKTKPREQFNSIFR	180
Qy	317	VWSVLTVYHODMLNGEYKCKCYKSNKGLPAPLEKITSKTKGQPREPQVYTLPPRSSEMTKN	376
Db	181	VWSVLTVYHODMLNGEYKCKCYKSNKGLPAPLEKITSKTKGQPREPQVYTLPPRSSEMTKN	240
Qy	377	QVSLTCLVKGFTYSDIAVEMESNGQRENNYKTPPMLDSDSFLYSKLTVDKSRMQGN	436
Db	241	QVSLTCLVKGFTYSDIAVEMESNGQRENNYKTPPMLDSDSFLYSKLTVDKSRMQGN	300
Qy	437	VFSCSVNHEALNHNHYQKSLSPGK	462
Db	301	VFSCSVNHEALNHNHYQKSLSPGK	326

RESULT 2

IG gamma-4 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 02-Apr-1992 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C/Accession: A90933; A90249; A02150
R/Elliott, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A/Reference number: A90933; MUID:83157104; PMID:6299662
A/Accession: A90933
A/Molecule type: DNA
A/Residues: 1-327 <Ell>
A/Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A/Note: The sequence was determined from the germ-line gene
R/Pink, J.R.L., Buttery, S.H.; De Vries, G.M.; Milestein, C.
Biochem. J. 117, 33-47, 1970
A/Title: Human immunoglobulin sublasses: Partial amino acid sequence of the constant
A/Reference number: A90249; MUID:70207560; PMID:4192699
A/Accession: A90249

A: Molecule type: protein
A: Residues: 1-30; 81-326 <PIN>
A: Cross-references: UNIPARC:UPI0000173795, UNIPARC:UPI0000173796
C: Genetics:
A: Gene: GDB:IGHG4
A: Cross-references: GDB:119340, OMIM:147130
A: Map position: 14q32.33-14q32.33
A: Introns: 99/1, 111/1, 221/1
C: Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C: Superfamily: immunoglobulin C region; immunoglobulin homology
C: Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F: 20-85/Domain: immunoglobulin homology <IM1>
F: 99-110/Region: hinge
F: 134-203/Domain: immunoglobulin homology <IM2>
F: 240-307/Domain: immunoglobulin homology <IM3>
F: 14/Disulfide bonds: interchain (to light chain) #status experimental
F: 27-83, 141-201, 247-305/Disulfide bonds: #status predicted
F: 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F: 177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	64.5%	Score 1605.5;	DB 1;	Length 327;
Best Local Similarity	92.4%;	Pred. No. 7.9e-86;		
Matches 302;	Conservative 10;	Mismatches 14;	Indels 1;	Gaps 1

Qy	137	ASRKGSGVPEPLPCSRGSTRSESTPAALGCVKQVPEPPELVSVNNSGALTSIGVTHFAVLQSS	156
Db	1	ASRKGSGVPEPLPCSRGSTRSESTPAALGCVKQVPEPPELVSVNNSGALTSIGVTHFAVLQSS	60
Qy	197	GLYSLSVVTVTVSSNFGIOTTYCNDADKPSNTKVDKTYERCCVCEGPCPCAPP-VAGPSV	255
Db	61	GLYSLSVVTVTVSSSISGKTQTYCNDADKPSNTKYDKRSEKTYGPPCSPCAPPEFLGPPSV	120
Qy	256	FLPEPRKQDTLISRPEVTCVVDVSHEDPEVQFNNVVDGEVHNKAKTRPREQFQSTF	315
Db	121	FLPEPRKQDTLISRPEVTCVVDVSDGEDEPQFNNVVDGEVHNKAKTRPREQFQSTY	180
Qy	316	RVISVULTVVAOWMLNGKEYKCVSNKGLPAPIEKTISTKQCPREPOVYLLPREAREMTK	375
Db	181	RVISVULTVVAOWMLNGKEYKCVSNKGLPSSIEKTISTAKQCPREPOVYLLPREQERMTK	240
Qy	376	NOVSLTCLVKGFPSPDIAVEMESNQPPNNKKTTPPMLDSDGSEFLYSKLTVDKSRMQQ	435
Db	241	NOVSLTCLVKGFPSPDIAVEMESNQPPNNKKTTPPVLDSGSEFLYSRLTVDKSRMQQ	300
Qy	436	NVFGSCVMHEALHNHYTKQSLSLSGK	462
Db	301	NVFGSCVMHEALHNHYTKQSLSLSGK	327

RESULT 3

Ig gamma-1 chain C region - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1991 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
 C/Accession: A93433; S36861; S33887; B90563; A90564; B91688; A91723; A02146
 R/Elliison, J.W.; Bersom, B.J.; Hood, L.E.
 Nucleic Acids Res. 10, 4071-4079, 1982
 A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
 A/Reference number: A93433; MUID:82274238; PMID:6287432
 A/Accession: A93433
 A/Molecule type: DNA
 A/Residues: 1-330 <EHL>
 A/Cross-references: UNIPROT:P01857, UNIPARC:UPI0000034C0E; EMBL:Z17370
 A/Note: this sequence has the Gm(17) allotypic marker, 197-Lys, and the Gm(1) markers, R/Harris, L.J.
 Submitted to the EMBL Data Library, October 1992
 A/Reference number: S33904
 A/Accession: S36861
 A/Molecule type: DNA
 A/Residues: 2-330 <HAR>
 A/Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R.Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Homjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113,235-330 <TAK>
A:CROSS-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:217370
R.Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammae-immunoglobulin. VII. Amino acid sequen
A:Reference number: A50563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: Protein
A:Residues: 1-96, 'R', '98-135 <CUN>
A:CROSS-references: UNIPARC:UPI000017378D
A:Note: this sequence has the Gm(3) marker, 97-Arg
R.Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammae-immunoglobulin. VII. Amino acid sequen
A:Reference number: A50564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A50564
A:Molecule type: Protein
A:Residues: 136-154, 'Q', '156-165, 'Q', '167-176, 'Q', '178-194, 'N', '196-197, 'D', '199-238, 'E', '240,
A:CROSS-references: UNIPARC:UPI000017378E
A:Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met
R.Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: Protein
A:Residues: 1-94, 'Q', '36-96, 'K', '98-115, 'Q', '117-197, 'D', '199-238, 'D', '240, 'E', '242-268, 'E', '27
A:CROSS-references: UNIPARC:UPI000017378F
A:Note: this sequence has the Gm(17) and Gm(1) markers
R.Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:684994
A:Contents: myeloma protein KOI, disulfide bonds
A:Accession: A91723
A:Molecule type: Protein
A:Residues: 1-96, 'R', '98-197, 'D', '199-238, 'E', '240, 'W', '242-266, 'D', '268-271, 'D', '273-330 <SCH
A:CROSS-references: UNIPARC:UPI0000173790
A:Note: this sequence has the Gm(3) and Gm(non-1) markers
R.Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammae-immunoglobulin. X. Intrachain disulfid
A:Reference number: A50565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R.Draker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
endromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:CROSS-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-4q32.33
A:Intron: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental

F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 64.4%; Score 1604; DB 1; Length 330;
Best Local Similarity 91.2%; Pred. No. 9.8e-86;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;
QY 137 ASTKPSVFPPLAPSPRSSTSESTALGCIYKQVPEPEPVVSNVSGALTSVHTFPAVLQSS 196
DB 1 ASTKPSVFPPLAPSPRSSTSESTALGCIYKQVPEPEPVVSNVSGALTSVHTFPAVLQSS 60
QY 197 GLYSLSVTVTPSSNFGTQYTCVNDHKNSTKVDKVERKCYE--CPGPCAPP-VAG 252
DB 61 GLYSLSVTVTPSSNFGTQYTCVNDHKNSTKVDKVERKCYE--CPGPCAPP-VAG 120
QY 253 PSVTLFPKPKDPTLMISTPTEPVTCVVDVSHEDBEVQPNVVDGVEVNNATKPREEPFN 312
DB 121 PSVTLFPKPKDPTLMISTPTEPVTCVVDVSHEDBEVQPNVVDGVEVNNATKPREEPFN 180
QY 313 STFRVSVTLVVDHDMNGEKYCKVSNKGPAPLEKTIKTKGQPREQVYTLPPSRR 372
DB 181 STFRVSVTLVVDHDMNGEKYCKVSNKGPAPLEKTIKTKGQPREQVYTLPPSRR 240
QY 373 MTKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPMLDSGFFYSKLTVDKSRW 432
DB 241 LTKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPMLDSGFFYSKLTVDKSRW 300
QY 433 QCGVVFSGSVHAEALHNTYTKSLSLSPGK 462
DB 301 QCGVVFSGSVHAEALHNTYTKSLSLSPGK 330
RESULT 4
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
A:Accession: S37483
R.Ducancel, F.P.D.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:CROSS-references: UNIPARC:UPI00002PB47; EMBL:X70423; MUD:9406252; PIDN:CAA49868.1; PI
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>
Query Match 64.2%; Score 1599.5; DB 2; Length 469;
Best Local Similarity 65.1%; Pred. No. 2.6e-85;
Matches 306; Conservative 60; Mismatches 95; Indels 9; Gaps 5;
QY 1 MECSVWMLFSLSGAGVLSVYOLQSGPELVKPGASVMSKASGYGTDYIHMVKQSH 60
DB 1 MECSVWMLFSLSGAGVLSVYOLQSGPELVKPGASVMSKASGYGTDYIHMVKQSH 60
QY 61 GKSLEWIGYIYPNNGNGYNOKFKGKATLTVDKSSSTAYMBELRTLTSDSAVYYCGR--- 117
DB 61 GQGLKMGWIMYPAAGNTRKYNENFKGKATLTVDSSSTAYVMSLTSDTAIVYFCARLWG 120
QY 118 STMDPFDYWGCGTTLTVSSASATKPSVPLAPPCRSRSTSESTALGCIYKQVPEPEPVTVSW 177
DB 121 ATATLTDWGGGTLTVSSASATKPSVPLAPVCGDITGSSVTLCGLVKGFPPEPVTLTW 180
QY 178 NSGALTSVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCVNDHKNSTKVDKVERK 237
DB 181 NSGALTSVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCVNDHKNSTKVDKVERK 239
QY 238 --CVCVCECP--CPAPP-VAGPSVTLFPKPKDPTLMISTPTEPVTCVVDVSHEDBEVQPNV 292

F.231-340/Domain: C2 region <CH3>
 F.341-446/Domain: C3 region <CH3>
 F.360-427/Domain: immunoglobulin homology <IM3>
 F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F.12-96,144-159,261-321,367-425/Disulfide bonds: #status predicted
 F.133/Disulfide bonds: interchain (to light chain) #status predicted
 F.224,227,229/Disulfide bonds: interchain #status predicted
 F.297/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 62.2%; Score 1549; DB 2; Length 446;
 Best Local Similarity 65.3%; Pred. No. 2e-82;
 Matches 292; Conservative 58; Mismatches 91; Indels 6; Gaps 4;

QY 20 EVOLQSGPELVKPGASVYMSKASGYGTDYTHMMQSHKSEMIQYTPNNKNGY 79
 DB 1 QIOLQSGPELVKPGASVYMSKASGYGTDYTHMMQSHKSEMIQYTPNNKNGY 60
 QY 80 NQKFGKATLVYDKSSSTAYMELRTLTSSESAVYCGSTWDDPDYWGQGTLLVYSSAST 139
 DB 61 NEKFGKATLVYDSSSTAYMQLSSLTSEDSAVYFCAGKGRAMDYWGQGTSTVYSSAKT 120
 QY 140 KQPSVPLAPGCRSTSESTALGCLVQYFPEPVYVSNKSGALTSGLTFPRAVLOSGLY 199
 DB 121 TAPSVYPLAPVCGDVTGSSVTLGCLVKGYPPEPVTLVNSGSLSSGVHTFPVALQSD-LY 179
 QY 200 SLSSVYVTPSSNFGQYGTQVNDHKNPTKVDKTVBERK--CCVEGPP--CPAPV-VAGPS 254
 DB 180 TLSSSVYVTPSSNFGQYGTQVNDHKNPTKVDKTVBERK--CCVEGPP--CPAPV-VAGPS 239
 QY 255 VFLPPEKPDYTLMSRTPEVTCVVDVSHEDPEVQFNMYVDGVEVNAKTKPREQFNST 314
 DB 240 VFIFPKIKDVLMLISLSPVTCVVDVSHEDPEVQFNMYVDGVEVNAKTKPREQFNST 299
 QY 315 FRVSVVLTVVHODMNGKRYCKKVSNGKLPAPIEKTISTKQCPPEPVYTLTPREBEMT 374
 DB 300 LRVASALPIQHDMMSGKFKCKVANNKDLPAIERITISKPKGSVAPQVYVLPPEBEMT 359
 QY 375 KNOVSLTCLVNGFYSDIYAVEMESNGQPENNYKTPPMIDSGSPFLVSKLTVDSRRMQ 434
 DB 360 KKQVTLTVNDVDFWEDIVETVNTNNGKTELTAKTEPVLDSGYSFMSKLVKKNAWE 419
 QY 435 GNVFSCSVHHEALHNHYTQKSLSPG 461
 DB 420 RNSYSCSVHHEALHNHYTQKSLSPG 446

RESULT 8
 G2MS11
 Ig gamma-2b chain - mouse
 CSpecies: Mus musculus (house mouse)
 CDate: 31-Mar-1980 #sequence revision 01-Dec-2000 #text_change 09-Jul-2004
 CAccession: S25057; A26235; A26233; A53598
 R.Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.U.; Kreuzaler, F.
 submitted to the EMBL Data Library, July 1992
 A.Description: Production of a Tobacco mosaic virus (TMV) inactivating neocorp specific m
 A.Accession: S25057
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-474 <FIS-
 A.Cross-references: UNIPROT: P01866; UNIPARC:UPI0000116095; EMBL:X67210; NID:G54826; PIDN
 R.Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Horio, T.
 Nature 283, 786-789, 1980
 A.Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
 A.Reference number: A02157; MUID:80120716; PMID:6766534
 A.Contents: a allele
 A.Accession: A02157
 A.Molecule type: DNA
 A.Residues: 138-161, 'L', 163-189, 'P', 193-474 <YAM>
 A.Cross-references: UNIPARC:UPI0000272D2; GB:J00461
 A.Note: the sequence was determined from the germ-line gene
 R.Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979

A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
 A.Reference number: A26235; MUID:80081501; PMID:117548
 A.Contents: MPC 11
 A.Accession: A26235
 A.Molecule type: mRNA
 A.Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU1>
 A.Cross-references: UNIPARC:UPI00001737AF
 A.Note: Lys-474 is probably removed posttranslationally
 R.Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
 A.Reference number: A26232; MUID:80081502; PMID:117549
 A.Accession: A26232
 A.Molecule type: DNA
 A.Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU2>
 A.Cross-references: UNIPARC:UPI00001737AF
 R.Ollo, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A>Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
 A.Reference number: A26233; MUID:82173203; PMID:6803173
 A.Contents: b allele
 A.Accession: A26233
 A.Molecule type: DNA
 A.Residues: 138-161, 'L', 163-189, 'P', 193-300, 'R', 302-331, 'A', 333-437, 'D', 440-474 <OLI>
 A.Cross-references: UNIPARC:UPI00001737B0; GB:J00461
 R.Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Iimura, T.; Takahash
 J.Biol. Chem. 269, 12345-12350, 1994
 A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A.Reference number: A53598; MUID:94216359; PMID:7512967
 A.Accession: A53598
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 234-251 <KIM>
 A.Cross-references: UNIPARC:UPI00001737B1
 A.Comment: The a allele sequence is shown.
 C.Genetics:
 A.Introns: 138/1; 236/1; 258/1; 368/1
 C.Comment: An immunoglobulin heterodimer subunit consists of two identical light (kap
 b) disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C.Superfamily: immunoglobulin C region; immunoglobulin homology
 C.Keywords: alternative splicing; duplication; glycoprotein; heterodimer; immunoglob
 F.157-222/Domain: immunoglobulin homology <IM1>
 F.236-257/Region: hinge
 F.281-350/Domain: immunoglobulin homology <IM2>
 F.387-454/Domain: immunoglobulin homology <IM3>
 F.152/Disulfide bonds: interchain (to light chain) #status predicted
 F.164-220,288-348,394-452/Disulfide bonds: #status predicted
 F.247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F.324/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 62.0%; Score 1545; DB 1; Length 474;
 Best Local Similarity 62.4%; Pred. No. 3.7e-82;
 Matches 296; Conservative 60; Mismatches 106; Indels 12; Gaps 4;

QY 1 MECSVWMLFLSSTAGVSEVQLOQSGPELVKPGASVYMSKASGYGTDYTHMMQSH 60
 DB 1 MECSVWMLFLSSTAGVSEVQLOQSGPELVKPGASVYMSKASGYGTDYTHMMQSH 60
 QY 61 GKSLEWIGYIPNNGNGYNOKFKGKATLVYDKSSSTAYMELRTLTSSESAVYCGRS-T 119
 DB 61 GKSLEWIGYIPNNGNGYNOKFKGKATLVYDKSSSTAYMELRTLTSSESAVYCGRS-T 119
 QY 120 WDDPYYWGQGTLLVYSSASTYKSPVPLAPGCRSTSESTALGCLVQYFPEPVYVSNWS 179
 DB 120 WDDPYYWGQGTLLVYSSASTYKSPVPLAPGCRSTSESTALGCLVQYFPEPVYVSNWS 179
 QY 121 YDWFYWGQGTLLVYSSASTYKSPVPLAPGCRSTSESTALGCLVQYFPEPVYVSNWS 180
 DB 121 YDWFYWGQGTLLVYSSASTYKSPVPLAPGCRSTSESTALGCLVQYFPEPVYVSNWS 180
 QY 180 GALTSGVTPPAVYQSGVLSVYVTPSSNFGQYGTQVNDHKNPTKVDKTVBERK 235
 DB 180 GALTSGVTPPAVYQSGVLSVYVTPSSNFGQYGTQVNDHKNPTKVDKTVBERK 235
 QY 236 ----RKC--CYECPCPAPV-AGPSVLPFPKPKDYLMSRTPEVTCVVDVSHEDPEV 288
 DB 236 ----RKC--CYECPCPAPV-AGPSVLPFPKPKDYLMSRTPEVTCVVDVSHEDPEV 288
 QY 241 ISTINPCPCCKCHKCPAPNLEGGSVIFPPNIDVLMISLTPVTCVVDVSHEDPEV 300
 DB 241 ISTINPCPCCKCHKCPAPNLEGGSVIFPPNIDVLMISLTPVTCVVDVSHEDPEV 300

[illegible]

RESULT 9
S01321
Ig gamma-2b chain precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C/Accession: S01321
R/de Waale, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Piers, W.
Eur. J. Biochem. 176, 287-295, 1988
A>Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A/Reference number: S01320; MUID:88329081; PMID:3138116
A/Accession: S01321

A:Residues: 1-175
A:Cross-references: UNIPARC:UPI000011SD8; EMBL:X13188; NTD:G51780; PTDN:CAA31580.1; PITH:
A>Note: this sequence was determined from the differentially expressed gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match	59.9%	Score 1490.5	DB 2	Length 475
Best Local Similarity	60.7%	Pred. No. 52e-79		
Matches 289	Conservative 66	Mismatches 106	Indels 15	Gaps 5

```

0Y 1 HBCSCVMLPFLJSTGAVJSEVOLQOSGBELPKASVMSCKASGJYTDYJYIMHMQSH 60
0Y 1 MEMWIFLFIJSTGAVQSOVOLQOSGAELARPASVJLSCASGJYTTISYGISWVKQRT 60
Db 1 MEMWIFLFIJSTGAVQSOVOLQOSGAELARPASVJLSCASGJYTTISYGISWVKQRT 60
0Y 61 GKSLWEMIGYIYIPNNNGNNGYNOKFKGKATLLTYDKSSSTAYMELRILTSDSDANVYCG--R 117
0Y 61 GKSLWEMIGYIYIPNNNGNNGYNOKFKGKATLLTYDKSSSTAYMELRILTSDSDANVYCG--R 117
Db 61 GQGLEWEMIGYIYIPGSSNSYFNEKFKGATLLTYDKSSSTAYMELRILTSDSDANVYCGAPGRQ 120
0Y 118 STWDFDYMGQGTLLTYVSSASTKGPSPVPLAPCSHSTSESTAAAGCLVKODFFPPRYTSM 177
Db 121 VGLRPFYMGQGTLLTYVSSASTKGPSPVPLAPCSHSTSESTAAAGCLVKODFFPPRYTSM 180
0Y 178 NSGALTSQVHTPPAVLQSSGLYSLSVVTVPSNSFGTYQTYTCNDHKSNTKVDYVE-- 235
Db 181 NSGSLSSSVHTFEPALLO--SGLYTWSSSVTVSSSTWPSQTYCVCSVAHPASSTTVVKKLEPS 239
0Y 236 -----RC--CVEBCPPAPPV-AGSPVFLPFPKXTLMSIRPRTKTVVNDVSHDP 286
Db 240 GPTSTINPCPPCKCHKCPAPMLBGSPVFLPFPKIKOVLMSLTPKXTCVVNDVSDPD 299
0Y 287 EVOFNMYVDYGEVHNHAKTPREBOFNSTFRVVSVTVVHODMLNKEKVCYVNSKGLPAP 346
Db 300 DVQJSMFANNVEVLTAOTQTHREDYNSLIRVVSALPIQHODMSKEKCKVNNKDLAP 359
0Y 347 IERTISKTKQGRBPOVYTLPPSRBEMTKNOVSLTCLVKGFPSPDIAYEWESNQCPENNY 406
Db 360 IERTISKTKGIVARAPQVYTLSPPPQOLSRKOVSLTCLVKGFPSPDIAYEWESNGTTEBNY 419
0Y 407 KTTPEMLSDSGFFLYSKLTVDXSRWQGNVSSCVMAEBALNHNTQSLSPK 462
Db 420 KOTAVLSDSGFFLYSKLNMKTSKMEKTDSSCNVREBGLNLYLKTITRSRPK 475

```

RESULT 10

S22080
Ig heavy chain precursor (B/M/T_4A.17.H5.A5) - bovine
N/Alternate names: Ig gamma-1 chain C region (clone 8.10)
C/Species: Bos primigenius taurus (cattle)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S22080, S06610, A31303
R/Sanders, P.C.
submitted to the EMBL Data Library, November 1991

A:Cross-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:q439; PDB:CAA44699.1; PDB:R:Symon, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A:Reference number: S06610; MUID:90097956; PMID:2513487
A:Accession: S06610

A: Molecule type: DNA
A: Residues: 142-470 <SYM>
A: Cross-references: UNIPARC:UPI0000176F36; EMBL:X16701
A: Note: the sequence was determined from the germline gene

C1Gene: Ig CH gamma-1
C1Introns: 98/1; 111/1; 221/1
C1Superfamily: immunoglobulin C region; immunoglobulin homology
C1Keywords: glycoprotein, heterotrimer; immunoglobulin; membrane protein
P161-225/Domain: immunoglobulin homology <1MM>
F131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	59.5%	Score 1481	DB 2	Length 470
Best Local Similarity	60.0%	Pred. No. 1.8e-78		
Matches 281	Conservative	65	Indels 16	Gaps 6

[illegible]

RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
CISpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
CDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

Db 120 VEGYGGYRFRHSGOCTLVTS-----EP- 144
Qy 174 TVSNNSGALTSGVHTFPVAVLGSSGLSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKT 233
Db 145 -----KSGCDKTH----- 151
Qy 234 VERRKCCVECPPCPPAP-VAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNW 292
Db 152 -----TCPCPAPAPLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNW 204
Qy 293 YVDGVEVNAKTKPREBOFNSTFRVSVTVTVHODMLNGEKYCKVSNKGLPAPIEKTIS 352
Db 205 YVDGVEVNAKTKPREBOFNSTFRVSVTVTVHODMLNGEKYCKVSNKGLPAPIEKTIS 264
Qy 353 KTKGQPREPOVYTLTPRSREEMTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTTPM 412
Db 265 KAKGQPREPOVYTLTPRSREEMTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTTPV 324
Qy 413 LQSDGSFFLYSKLTVDKSRWQQGNVFSQVMEHRLAHNYTOKSLISLSPGK 462
Db 325 LQSDGSFFLYSKLTVDKSRWQQGNVFSQVMEHRLAHNYTOKSLISLSPGK 374

RESULT 14

147159
Ig gamma 2a chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47159
R/Kaczkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PI
A/Genes: IGG2a
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F.133-202/Domain: immunoglobulin homology <IMM>

Query Match 51.0%; Score 1271; DB 2; Length 328;
Best Local Similarity 70.4%; Pred. No. 1.6e-66;
Matches 231; Conservative 40; Mismatches 55; Indels 2; Gaps 1;
Qy 137 ASTKGSVPPLAPCSRSTSESTALGCLVKDYFPPPVTVSNNSGALTSGVHTFPVAVLGSS 196
Db 1 AKTAPLVYPLAPCGSDTSGPNVALGCLASSYFPPEVTVTVNSGALTSGVHTFPVAVLGSS 60
Qy 197 GLYSLSNVTVPPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKCCVECPPCPPAPVAGPSVF 256
Db 61 GLYSLSNMTVPPASSLSKSYTCNVNHPATTTKVDKRGVGTKKPPCPCPACSPGSPSVF 120
Qy 257 LPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 316
Db 121 IFPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 180
Qy 317 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLTPRSREEMTKN 376
Db 181 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLTPRSREEMTKN 240
Qy 377 QVSLTCLVKGFYPSDIAVWESNNGQ--PENNYKTTTPMLDSGFFLYSKLTVDKSRWQQ 434
Db 241 KVSITCLVIGFPPDIVEMQNGQPREPGNRTTTPQDDVDGTYFLYSKFSVDASNGG 300
Qy 435 GNVFSCSVMEHRLAHNYTOKSLISLSPGK 462
Db 301 GGIFQCAVMHEALAHNYTOKSLISLSPGK 328

RESULT 15

147160
Ig gamma 2b chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47160
R/Kaczkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PI
A/Genes: IGG2b
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F.133-202/Domain: immunoglobulin homology <IMM>

Query Match 50.8%; Score 1265; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 3.6e-66;
Matches 230; Conservative 39; Mismatches 57; Indels 2; Gaps 1;
Qy 137 ASTKGSVPPLAPCSRSTSESTALGCLVKDYFPPPVTVSNNSGALTSGVHTFPVAVLGSS 196
Db 1 AKTAPLVYPLAPCGSDTSGPNVALGCLASSYFPPEVTVTVNSGALTSGVHTFPVAVLGSS 60
Qy 197 GLYSLSNVTVPPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKCCVECPPCPPAPVAGPSVF 256
Db 61 GLYSLSNMTVPPASSLSKSYTCNVNHPATTTKVDKRGVGTKKPPCPCPACSPGSPSVF 120
Qy 257 LPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 316
Db 121 IFPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 180
Qy 317 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLTPRSREEMTKN 376
Db 181 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLTPRSREEMTKN 240
Qy 377 QVSLTCLVKGFYPSDIAVWESNNGQ--PENNYKTTTPMLDSGFFLYSKLTVDKSRWQQ 434
Db 241 KVSITCLVIGFPPDIVEMQNGQPREPGNRTTTPQDDVDGTYFLYSKFSVDASNGG 300
Qy 435 GNVFSCSVMEHRLAHNYTOKSLISLSPGK 462
Db 301 GGIFQCAVMHEALAHNYTOKSLISLSPGK 328

Search completed: January 24, 2006, 18:57:19
Job time : 33.3863 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:44:45 ; Search time 150.695 Seconds
(without alignment)
2163.001 Million cell updates/sec

Title: US-10-828-782a-18

Perfect score: 2490

Sequence: 1 MECSGWLFLSLGTAGVLSB.....MHEALHNHYTKSLSLSPGK 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2045	82.1	464	Q6MZU6_HUMAN	Q6MZU6 homo sapien
2	2035	81.7	470	Q6B6C4_HUMAN	Q6B6C4 homo sapien
3	2025.5	81.3	465	Q6B6C4_HUMAN	Q6B6C4 homo sapien
4	1962.5	78.8	469	Q727P5_HUMAN	Q727P5 homo sapien
5	1958	78.6	518	Q6N030_HUMAN	Q6N030 homo sapien
6	1955	78.5	417	Q6N093_HUMAN	Q6N093 homo sapien
7	1950.5	78.3	475	Q6N093_HUMAN	Q6N093 homo sapien
8	1942.5	78.0	519	Q6B6M2_HUMAN	Q6B6M2 homo sapien
9	1940	77.9	480	Q6B6F1_HUMAN	Q6B6F1 homo sapien
10	1924.5	77.3	465	Q6B6M6_HUMAN	Q6B6M6 homo sapien
11	1922.5	77.2	469	Q6B6F4_HUMAN	Q6B6F4 homo sapien
12	1922	77.2	472	Q6N089_HUMAN	Q6N089 homo sapien
13	1910.5	76.7	475	Q6B6E1_PONPY	Q6B6E1 pongo pygma
14	1909	76.7	470	Q6B6F4_HUMAN	Q6B6F4 homo sapien
15	1904	76.5	476	Q6B6M1_HUMAN	Q6B6M1 homo sapien
16	1903	76.4	478	Q6B6I8_HUMAN	Q6B6I8 homo sapien
17	1899.5	76.3	475	Q6B6E5_HUMAN	Q6B6E5 homo sapien
18	1898	76.2	475	Q6N096_HUMAN	Q6N096 homo sapien
19	1896.5	76.2	475	Q6N096_HUMAN	Q6N096 homo sapien
20	1895	76.1	466	Q6N096_HUMAN	Q6N096 homo sapien
21	1894.5	76.1	473	Q6N094_HUMAN	Q6N094 homo sapien
22	1882	75.6	480	Q6N094_HUMAN	Q6N094 homo sapien
23	1881	75.5	470	Q6N094_HUMAN	Q6N094 homo sapien
24	1877.5	75.4	475	Q6N094_HUMAN	Q6N094 homo sapien
25	1869.5	75.1	544	Q6B6J5_HUMAN	Q6B6J5 homo sapien
26	1860.5	74.7	473	Q6B6J5_HUMAN	Q6B6J5 homo sapien
27	1859	74.7	482	Q6B6J5_HUMAN	Q6B6J5 homo sapien
28	1853.5	74.4	481	Q6N097_HUMAN	Q6N097 homo sapien
29	1848	74.2	473	Q6N097_HUMAN	Q6N097 homo sapien
30	1841.5	74.0	521	Q6N097_HUMAN	Q6N097 homo sapien
31	1837	73.8	476	Q6N097_HUMAN	Q6N097 homo sapien

32	1755	70.5	326	1	IGHG2_HUMAN	P01859 homo sapien
33	1699	68.2	472	2	Q6B6J7_MOUSE	Q6B6J7 mus musculu
34	1676	67.3	348	2	Q6B6Y1_HUMAN	Q6B6Y1 homo sapien
35	1670.5	67.1	477	2	Q5B6E6_MOUSE	Q5B6E6 mus musculu
36	1655	66.5	470	2	Q7TMC1_MOUSE	Q7TMC1 mus musculu
37	1631.5	65.5	463	2	Q5B6J2_RAT	Q5B6J2 rattus norv
38	1606	64.5	458	2	IGHG4_HUMAN	P01861 homo sapien
39	1605.5	64.5	327	1	IGHG4_HUMAN	P01857 homo sapien
40	1604	64.3	330	1	IGHG1_HUMAN	Q559W9 mus musculu
41	1601	64.3	468	2	Q569W9_MOUSE	Q569W9 mus musculu
42	1588.5	63.8	473	2	Q9DBL4_MOUSE	Q9DBL4 mus musculu
43	1583.5	63.6	487	2	Q652L2_SMUR1	Q652L2 mus sp. tyv
44	1571.5	63.1	509	2	Q6N017_HUMAN	Q6N017 homo sapien
45	1569	63.0	458	2	Q5BK05_RAT	Q5BK05 rattus norv

ALIGNMENTS

Query Match	Score	DB 2:	Length	464:
Best Local Similarity	82.4%	Pred. No. 3.6e-134;		
Matches	383;	Conservative	33;	Mismatches 45;
Indels			4;	Gaps 3;
QY	1	MECSGWLFLSLGTAGVLSB.....MHEALHNHYTKSLSLSPGK	60	
DB	1	MELGIRWFLVALIEGVCEVQLVSSGGGLVPGSLSLSCASGFTSSSMNVRQAP	60	
QY	61	GKSLIEWIGYIPNNNGN--GYNOKFKGKATITVDKSSSTAYWELTTLTSEDVAVYCCGS	118	
DB	61	GKSLIEWIGYIPNNNGN--GYNOKFKGKATITVDKSSSTAYWELTTLTSEDVAVYCCGS	118	
QY	119	T-WDDFDYWGQGTTLTSSASTKGPVPLAPCSRSTSESTALACLYKDYFPEPVYTSW	177	
DB	120	LGMFLDLYWGGQGTTLTSSASTKGPVPLAPCSRSTSESTALACLYKDYFPEPVYTSW	179	
QY	178	NSGALTSGVHPRPVAVLQSSGLYSLSVTVPSNSNGTGTTCNVVDHKSNFTKVDKTVKX	237	

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Db      180 NSGALTSVHTPPAVLQSSGLYSLSVTVVSSNFGTQTCTCNVHKPNTKVTVERK 239
Qy      238 CCVECPCPAPVAGPSVFLPPKPKDPTLMISRTPEVTCVVVDVSHEDVEGFNNVYVDG 297
Db      240 CCVECPCPAPVAGPSVFLPPKPKDPTLMISRTPEVTCVVVDVSHEDVEGFNNVYVDG 299
Qy      298 EVHNAKTKPREQFNSTFRVSVLTGVHODMLNGEKYCKVSNKGLPAPIETKISKTKQ 357
Db      300 EVHNAKTKPREQFNSTFRVSVLTGVHODMLNGEKYCKVSNKGLPAPIETKISKTKQ 359
Qy      358 PREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPMLDSG 417
Db      360 PREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPMLDSG 419
Qy      418 SFFLYSKLTVDSKRMQGNVFSQVHMEALHNNHYTKSLSPGK 462
Db      420 SFFLYSKLTVDSKRMQGNVFSQVHMEALHNNHYTKSLSPGK 464

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RESULT 2

```

068CN4 HUMAN
ID      068CN4 HUMAN PRELIMINARY; PRT; 470 AA.
AC      068CN4;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE      Hypothetical protein DKFp668E23209.
GN      Name=DKFp668E23209;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Rectum tumor;
RG      The German cDNA Consortium;
RA      Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amlid C.,
RA      Osaenger A., Fobo G., Han M., Wiemann S.;
RA      Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR      EMBL; CR749861; CAH18705.2; -; mRNA.
DR      SMR; 068CN4; 43-493.
DR      GO; GO:0016021; C:Integral to membrane; IEA.
DR      InterPro; IPR003599; Iq.
DR      InterPro; IPR007110; Iq-1like.
DR      InterPro; IPR003597; Iq.C1.
DR      InterPro; IPR003006; Iq_MHC.
DR      InterPro; IPR003596; Iq_Y.
DR      Pfam; PF07654; C1-set; 3.
DR      SMART; SM00409; Iq; 2.
DR      SMART; SM00407; IqC1; 3.
DR      SMART; SM00406; IqC1; 1.
DR      PROSITE; PS50835; Iq_LIKE; 4.
DR      PROSITE; PS50830; Iq_MHC; UNKNOWN 2.
KW      Hypothetical protein.
SQ      SEQUENCE 470 AA; 51536 MW; 7CB061DFC03D0B2B CRC64;

```

Query Match 81.7%; Score 2035; DB 2; Length 470;

Best Local Similarity 81.5%; Pred. No. 1.8e-133;

Matches 383; Conservative 27; Mismatches 52; Indels 8; Gaps 2;

```

Qy      1 MECSQVMTFLLSGTAGVLSRVDLQSGPELVKRGASVKNSCRASGYTGDTYYIHMKQSH 60
Db      1 MEFGLSWVFLVALLRQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 60
Qy      61 GKSLEWIGIYYPNNGANGYNQKFKKATITVDKSSSTAYMEIRTLTSDSAVYYGCR--- 117
Db      61 GARLEWVAIVSYEGGQKHADSVKYGATISRDNSMKTYSIQLSGLSTEDTGYVYCARDEL 120
Qy      118 --STWDD--FDYMGQGTLLTVSSASTKGPVFPPLAPCSRSTSESTAAAGCIVKQYFPP 172
Db      121 PLSSHTNTYALVDVWGQGTAVIVSSASTKGPVFPPLAPCSRSTSESTAAAGCIVKQYFPP 180

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```

Qy      173 VTVSNISGALTSVHTPPAVLQSSGLYSLSVTVVSSNFGTQTCTCNVHKPNTKVTYDK 232
Db      181 VTVSNISGALTSVHTPPAVLQSSGLYSLSVTVVSSNFGTQTCTCNVHKPNTKVTYDK 240
Qy      233 TVERRCCVCPAPVAGPSVFLPPKPKDPTLMISRTPEVTCVVVDVSHEDVEGFNNVYVDG 292
Db      241 TVERRCCVCPAPVAGPSVFLPPKPKDPTLMISRTPEVTCVVVDVSHEDVEGFNNVYVDG 300
Qy      293 YVDGVEVNAKTKPREQFNSTFRVSVLTGVHODMLNGEKYCKVSNKGLPAPIETKISK 352
Db      301 YVDGVEVNAKTKPREQFNSTFRVSVLTGVHODMLNGEKYCKVSNKGLPAPIETKISK 360
Qy      353 KTKGQPREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPM 412
Db      361 KTKGQPREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKATPPM 420
Qy      413 LDSQSFYLSKLTVDKSRMOQGNVFSQVHMEALHNNHYTKSLSPGK 462
Db      421 LDSQSFYLSKLTVDKSRMOQGNVFSQVHMEALHNNHYTKSLSPGK 470

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RESULT 3

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068C4 HUMAN
ID      068C4 HUMAN PRELIMINARY; PRT; 465 AA.
AC      068C4;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE      Hypothetical protein.
GN      Name=DKFp668E23209;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RG      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA      Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA      Bock S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield J.S.N., Krzywicki M.T., Skalska U., Smialowski D.B.,
RA      Schnerch A., Schein J.B., Jones S.J.W., Marra M.A.;
RA      "Generation and initial analysis of more than 15,000 full-length human
RA      RT and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RG      Strausberg R.;
RA      Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC062335; AAH62335.1; -; mRNA.
DR      HSRP; P01861; IADQ.
DR      SMR; 068C4; 20-465.
DR      InterPro; IPR003599; Iq.
DR      InterPro; IPR007110; Iq-1like.
DR      InterPro; IPR003597; Iq.C1.
DR      InterPro; IPR003006; Iq_MHC.
DR      InterPro; IPR003596; Iq_Y.
DR      Pfam; PF07654; C1-set; 3.

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DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 465 AA; 51395 MW; FDD9348ADC37E6D CRC64;

Query Match 81.3%; Score 2025.5; DB 2; Length 465;
 Best Local Similarity 81.3%; Pred. No. 8.2e-133;
 Matches 378; Conservative 32; Mismatches 52; Indels 3; Gaps 1;

QY 1 MECSCWMLFLSAGTAVLSEVQLQSGPELVKPGASVMSCKASGYTDTYIHMMKQSH 60
 DB 1 MELGNWLVLAILEGVCCEVQLMSAGLVKPGSLSLSCASLSPFSEVMMSVVRQAP 60
 QY 61 GKSLWIGYIYPNNGNGYNOKFKKATLTVDKSSSTIAMELRITLSDSAVYTCGRSTW 120
 DB 61 GKLEWVANIKDDGATYHLDVSKGRFTISRDNANNTIYLQWNSLRVEDTAMYYCAREIP 120
 QY 121 DD---FDYWGQGTTLTVSSASTKGPSVFLPACSHSTSESTALGCLVKDYPEPEVTWS 177
 DB 121 GGRCTYDWMHGHTLVSSASTKGPSVFLPACSHSTSESTALGCLVKDYFPEPEVTWS 180
 QY 178 NSGALTSGVHTFPAVLQSSGLYSLSVTVVPSSNFGTQTYTCNVDHKPSNTKVDKTVBRK 237
 DB 181 NSGALTSGVHTFPAVLQSSGLYSLSVTVVPSSNFGTQTYTCNVDHKPSNTKVDKTVBRK 240
 QY 238 CCVECPCPAPVAGPSVFLPFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQNNYVDGV 297
 DB 241 CCVECPCPAPVAGPSVFLPFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQNNYVDGV 300
 QY 298 EVHNAKTPREBOFNSTFRVSVLVTVHODMLNGEKYCKVSNKGLPAPIETKTSKTQ 357
 DB 301 EVHNAKTPREBOFNSTFRVSVLVTVHODMLNGEKYCKVSNKGLPAPIETKTSKTQ 360
 QY 358 PREPOVYTLPPSREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPMLDSG 417
 DB 361 PREPOVYTLPPSREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPMLDSG 420
 QY 418 SFFLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSLSPGK 462
 DB 421 SFFLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSLSPGK 465

RESULT 4
 Q727P5 HUMAN PRELIMINARY; PRT; 469 AA.

AC 0727P5;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide P.,
 RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC051328; AAH51328.1; mRNA.
 DR HSSP; P01857; 1H2H.
 DR SMR; Q727P5; 20-469.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Immunoglobulin domain
 SQ SEQUENCE 469 AA; 51395 MW; C6D5BE12BAAP795C CRC64;

Query Match 78.8%; Score 1962.5; DB 2; Length 469;
 Best Local Similarity 78.5%; Pred. No. 2.1e-128;
 Matches 368; Conservative 42; Mismatches 52; Indels 7; Gaps 3;

QY 1 MECSCWMLFLSAGTAVLSEVQLQSGPELVKPGASVMSCKASGYTDTYIHMMKQSH 60
 DB 1 MDWTMSILFLVAATGAPQVHLVQSGAEVKKPGASVLTCKTSGYNSYDLIWRQAP 60
 QY 61 GKSLWIGYIYPNNGNGYNOKFKKATLTVDKSSSTIAMELRITLSDSAVYTC---GR 117
 DB 61 GQLEWVANIKDDGATYHLDVSKGRFTISRDNANNTIYLQWNSLRVEDTAMYYCAREIP 120
 QY 118 STWDDFDYWGQGTTLTVSSASTKGPSVFLPACSHSTSESTALGCLVKDYPEPEVTWS 177
 DB 121 GQVDFPDMGQGTTLTVSSASTKGPSVFLPACSHSTSESTALGCLVKDYPEPEVTWS 180
 QY 178 NSGALTSGVHTFPAVLQSSGLYSLSVTVVPSSNFGTQTYTCNVDHKPSNTKVDKTVBRK 237
 DB 181 NSGALTSGVHTFPAVLQSSGLYSLSVTVVPSSNFGTQTYTCNVDHKPSNTKVDKTVBRK 240
 QY 238 CCVE---CPGCPAPVAGPSVFLPFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQNNY 293
 DB 241 SCDKTHCTCPGCPAPVAGPSVFLPFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFQNNY 300
 QY 294 VDGVEVHNAKTPREBOFNSTFRVSVLVTVHODMLNGEKYCKVSNKGLPAPIETKTSK 353
 DB 301 VDGVEVHNAKTPREBOFNSTFRVSVLVTVHODMLNGEKYCKVSNKGLPAPIETKTSK 360
 QY 354 TKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPML 413
 DB 361 AKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPML 420
 QY 414 DSDGSFPLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSLSPGK 462
 DB 421 DSDGSFPLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSLSPGK 469

RESULT 5

Q6N030 HUMAN PRELIMINARY; PRT; 518 AA.
 AC Q6N030;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686i15212.

GN Name=DKFZp686i15212;

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_TaxID=9606;

RM (1)

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Rectum tumor;

RG The German cDNA Consortium;

RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640724; CAE45841.1; -; mRNA.

DR HSSP; P01861; IADQ.

DR InterPro; IPR000005; HTHARAC.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 3.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

DR Hypothetical protein.

KW Hypothetical protein.

SO SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match 78.6%; Score 1958; DB 2; Length 518;

Best Local Similarity 73.0%; Pred. No. 4,8e-128;

Matches 378; Conservative 37; Mismatches 47; Indels 56; Gaps 5;

1 MECSVMFLSLSTAGVLSVVOLOQSGPFLVPGASVYKMSCTASGTGTDYIIMMKOSH 60

1 MDMTRILFLVLAATGAHSGVHLVOSGAEVKKPGASVKSCTASGYPFTNHINWRCAP 60

61 GKSLEWIGYIYPNNGNGVNGKFKGKATLTVDKSSSTAYMETRLTSDSAVYCGRS-- 118

61 GQSLWEMGINTGNGTKYSQKFGQVITTRDTMTTAAJLSSLSSTEDTAVYWCARDAP 120

119 ---TWDDPDYWGQITLTVSSASTKGPVFPPLAPCSRSTSESTALGLVNDYFPEPV 175

121 GQVTTTTPDYWGQITLTVSSASTKGPVFPPLAPCSRSTSESTALGLVNDYFPEPV 180

176 SNWSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSNTKDKTVE 235

181 SNWSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSNTKDKTVE 240

236 RK-----C--CYE-----CPRC 245

241 LKTPVADTHTTCPCRCPEKPCDTPPCRCPEKSCDTPPCRCPEKSCDTPPCRCPC 300

246 PAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPVQFMVYDGEVNAKT 304

301 PAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPVQFMVYDGEVNAKT 360

305 KRRERQNSTFRVYVLTIVHODMLNGSKYCKVSNKGLPAPIEKTISTKQPREPVY 364

361 KRRERQNSTFRVYVLTIVHODMLNGSKYCKVSNKGLPAPIEKTISTKQPREPVY 420

365 TTPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPMI.DSGSFFLYSK 424

421 TTPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPMI.DSGSFFLYSK 480

425 LTVDKSRMQQGNVFSVHSEALHNHYTKSLISLSPGK 462

481 LTVDKSRMQQGNVFSVHSEALHNHYTKSLISLSPGK 518

RESULT 6

Q6N093_HUMAN

AC Q6N093;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686i04196 (fragment).

GN Name=DKFZp686i04196;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_TaxID=9606;

RM (1)

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Human esophagus tumor;

RG The German Human cDNA Consortium;

RA Wandt R., Heubner D., Meves H.W., Weil B., Amd C., Osanger A.,

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640623; CAR45777.1; -; mRNA.

DR HSSP; P01861; IADQ.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 3.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.

FT NON TER 1

SO SEQUENCE 417 AA; 46061 MW; C4518B844CFB883C CRC64;

Query Match 78.5%; Score 1955; DB 2; Length 417;

Best Local Similarity 87.5%; Pred. No. 5.9e-128;

Matches 363; Conservative 20; Mismatches 30; Indels 2; Gaps 1;

50 DYIIMMKQSHGKSLWYIYPNNGNGVNGKFKGKATLTVDKSSSTAYMETRLTSD 109

3 NYAMHMTVQAGKGLWYAVIAYDSQYVADSVGRFTVSRDNTLFLWMSLRDED 62

110 SAVVYCGR--STWDDPDYWGQITLTVSSASTKGPVFPPLAPCSRSTSESTALGLVND 167

63 TAVYTCALAHGSGTSKFDPMGQITLTVSSASTKGPVFPPLAPCSRSTSESTALGLVND 122

168 YFPEPVTVSNWSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSN 227

123 YFPEPVTVSNWSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSN 182

228 TKVDKTVRKCCVCECPAPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPV 287

183 TKVDKTVRKCCVCECPAPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPV 242

288 VQFNMYVGVVHNAKTPREERQNSTFRVYVLTIVHODMLNGSKYCKVSNKGLPAPI 347

243 VQFNMYVGVVHNAKTPREERQNSTFRVYVLTIVHODMLNGSKYCKVSNKGLPAPI 302

348 EKTISTKQPREPVYTLTPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYK 407

303 EKTISTKQPREPVYTLTPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYK 362

408 TTPPMLDSDGSFFLYSKLTVDKSRMQQGNVFSVHSEALHNHYTKSLISLSPGK 462

363 TTPPMLDSDGSFFLYSKLTVDKSRMQQGNVFSVHSEALHNHYTKSLISLSPGK 417

RESULT 7

Q6N093_HUMAN

ID Q6N095 HUMAN PRELIMINARY; PRT; 475 AA.
 AC Q6N095;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686K03196.
 GN Name=DKFZp686K03196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RP TISSUE=Esophagus tumor;
 RC The German cDNA Consortium;
 RA Wandtke R., Heubner D., Mewes H.W., Weil B., Amdt C., Ossanger A.,
 RA Fodor G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640621; CA645775.1; -, mRNA.
 DR HSSP; P01861; IADO.
 DR SMR; Q6N095; 20-475.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG.C1.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG.LIKE; 4.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;
 Query Match 78.3%; Score 1950.5; DB 2; Length 475;
 Best Local Similarity 79.2%; Pred. No. 1,4e-127;
 Matches 369; Conservative 37; Mismatches 47; Indels 13; Gaps 4;
 QY 10 LLSGAGVLSVVOLOQSGPBLVKGAVKMSCKASGVTGTDYYIHMKQSHKSLWIGY 69
 DB 10 LLAVALPGHLSQVQLVQSGAEIKRKPASVYISCRASGYSRSTVHIMVWQAPQRLWMMGI 69
 QY 70 IYPNNGGNGYNCKFKGKATLTVDKSSSTRAYMEIRLTLSDESAVYTC-----GRSTW---- 120
 DB 70 MNPBDSKTYAQTFOGRMTMTDTSTSTVFMEINLSKSGDTAVYVYCTDRSGRALMFGEL 129
 QY 121 DDFVWGGQTTLVSSASTKGPSVPLAPCSRSTSESTPAALGCLVKDYFPEPVTVSNMNG 180
 DB 130 DAFDWMGGQTKVTVSSASTKGPSVPLAPSSKSTSGTRALGCLVKDYFPEPVTVSNMNG 189
 QY 181 ALTSGVHTPFAVLQSSGLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKTVRKCVCV 240
 DB 190 ALTSGVHTPFAVLQSSGLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKVPKSCD 249
 QY 241 E---CPGPCPAPV-VAGPSVFLFPPPKKDTLMSKRPETVCVVVDVSHEDPEVQFWMYIDG 296
 DB 250 KHTPCPPCPAPBELLGGPSVFLFPPPKKDTLMSKRPETVCVVVDVSHEDPEVQFWMYIDG 309
 QY 297 VEVNAKAKPKREQGNSTFRVSVLTVAHQDLNGEKYCKSNGLPAPIKTIKSTKSG 356
 DB 310 VEVNAKAKPKREQGNSTFRVSVLTVAHQDLNGEKYCKSNGLPAPIKTIKSTKSG 369
 QY 357 QPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIAMVESNGCPENNYKTTTPMLDSD 416
 DB 370 QPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIAMVESNGCPENNYKTTTPMLDSD 429
 QY 417 GSFELYSKLTVDKSRWQGNVSCVMHAKLNNHTTKSLSPK 462
 DB 430 GSFELYSKLTVDKSRWQGNVSCVMHAKLNNHTTKSLSPK 475

RESULT 8
 ID Q5EBM2 HUMAN PRELIMINARY; PRT; 519 AA.
 AC Q5EBM2;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN Name=DKFZp686K03196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lymph.
 RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueadi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC089421; AA89421.1; -, mRNA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG.C1.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.V.
 DR Pfam; PF07654; CI-set; 3.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG.LIKE; 4.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 519 AA; 56813 MW; 988C5C2P92B9E34C CRC64;
 Query Match 78.0%; Score 1942.5; DB 2; Length 519;
 Best Local Similarity 72.3%; Pred. No. 5.8e-127;
 Matches 375; Conservative 34; Mismatches 53; Indels 57; Gaps 5;
 QY 1 MECSCTMLFLISGTRGVLSVVOLOQSGPBLVKGAVKMSCKASGVTGTDYYIHMKQSH 60
 DB 1 MDCWIRILLVAATGTAQVQLVQSGAEVKKPKGASVAVSCVSGHTLTLSRHWRQAP 60
 QY 61 GKSLEMIYGIYPPNNGGNGYNCKFKGKATLTVDKSSSTRAYMEIRLTLSDESAVYTCGRSTW 120
 DB 61 GKSLEMIYGIYPPNNGGNGYNCKFKGKATLTVDKSSSTRAYMEIRLTLSDESAVYTCGRSTW 120
 QY 121 D-----DPDYWGQTTLVSSASTKGPSVPLAPCSRSTSESTPAALGCLVKDYFPEPV 174
 DB 121 DVLNYSRFDYWGQTTLVSSASTKGPSVPLAPCSRSTSESTPAALGCLVKDYFPEPV 180

QY 175 VSMNGALISGVHTPPAVLOSGLYSLSVTVTPSSNFGTQTYTCNVHKKPENTIVDKTV 234
 DB 181 VSMNGALISGVHTPPAVLOSGLYSLSVTVTPSSNFGTQTYTCNVHKKPENTIVDKTV 240
 QY 235 EKK-----C-CV-----CPR 244
 DB 241 ELKTLPGDTTTCPCRCPEPKSCDTPPCRCPEPKSCDTPPCRCPEPKSCDTPPCPR 300
 QY 245 CPAPP-VAGPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVQFNYYVGVGVHNAK 303
 DB 301 CPAPELGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVQFNYYVGVGVHNAK 360
 QY 304 TKPREBQFNSTFRVSVLTVVHQMNGKRYCKVSNKGLPAPIEKTISKTKGQPREPOV 363
 DB 361 TKPREBQFNSTFRVSVLTVVHQMNGKRYCKVSNKGLPAPIEKTISKTKGQPREPOV 420
 QY 364 YTLPPSRBEMTKNOVSLTCLVNGFYPSDIAVEMESGQPENNYKTPMLDSDGSFFLYS 423
 DB 421 YTLPPSRBEMTKNOVSLTCLVNGFYPSDIAVEMESGQPENNYKTPMLDSDGSFFLYS 480
 QY 424 KLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 462
 DB 481 KLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 519

RESULT 9

06PUP1 HUMAN PRELIMINARY; PRT; 480 AA.

AC 06PUP1; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DB Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feihy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maitra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA Strausberg R.L.

Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC016381; AAH16381.1; -; mRNA.

DR HSSP; P01861; IADO.

DR InterPro; IPR003559; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG_c1.

DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; Cl-sect; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;

Query Match 77.9%; Score 1940; DB 2; Length 480;
 Best Local Similarity 77.3%; Pred. No. 7.8e-127;
 Matches 371; Conservative 35; Mismatches 56; Indels 18; Gaps 4;

QY 1 MECSVMFLSGLTGVLSVLOQSGPELVFGASVMSQCAAGTGYTHMKQSH 60
 DB 1 MDWTRFLFVVAALAGVSOQLVQSGAEVKKRGSVAVSCASGSGSGSFISVVRQAP 60
 QY 61 GKSLKEMIGYIPNNGNGNGNOKFKGKATLVDKSSSTAYMELRTLTSEDNAVYTCR--- 117
 DB 61 GGGLAMWGIIIPAFDITKAGNFODRVITISADESTDTAYMELRSRSEDATYYCARDLA 120
 QY 118 --STWDDF-----DYQGQTLTVSSASTKPSVFPPLAPCSRSTSESTAAIGLVK 166
 DB 121 LVELMSGFHTDEKYYGLVWVGQGPVTVSSATKPSVFPPLAPSSKSTSGGTAALGCLVK 180
 QY 167 DYFPPVTVSMNSGALTSQVHTFPVAVLOSGLYSLSVTVTPSSNFGTQTYTCNVHKKPS 226
 DB 181 DYFPPVTVSMNSGALTSQVHTFPVAVLOSGLYSLSVTVTPSSNFGTQTYTCNVHKKPS 240
 QY 227 NTKVDKTKERKCCV---CPRCPAPP-VAGPSVFLPPPKKDTLMISRTPEVTCVVDVS 282
 DB 241 NTKVDKTKERKCCV---CPRCPAPP-VAGPSVFLPPPKKDTLMISRTPEVTCVVDVS 300
 QY 283 HEDPEVQFNYYVGVHNAKTKPREBQFNSTFRVSVLTVVHQMNGKRYCKVSNKGL 342
 DB 301 HEDPEVQFNYYVGVHNAKTKPREBQFNSTFRVSVLTVVHQMNGKRYCKVSNKGL 360
 QY 343 LPAPIEKTISKTKGQPREPOVTVLPPSRBEMTKNOVSLTCLVNGFYPSDIAVEMESGQ 402
 DB 361 LPAPIEKTISKTKGQPREPOVTVLPPSRBEMTKNOVSLTCLVNGFYPSDIAVEMESGQ 420
 QY 403 ENNYKTPMLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 462
 DB 421 ENNYKTPMLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 480

RESULT 10

06GKX6 HUMAN PRELIMINARY; PRT; 465 AA.

AC 06GKX6; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DB Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sect; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 77.3%; Score 1924.5; DB 2; Length 465;
Best Local Similarity 78.9%; Pred. No. 9e-126;
Matches 362; Conservative 37; Mismatches 55; Indels 5; Gaps 3;

QY 8 LFLISGTAGVLSVVOLOSGPELVKPGASVWMSCKASGYGTIDYIHMKQSHGKSLMI 67
DB 8 LILVAPRWVLSQVLOSGPELVKPGASVWMSCKASGYGTIDYIHMKQSHGKSLMI 67
QY 68 GIYVNNNGNGYNOQFKGKATLVVKSSTAYMEIRLTLSSEDAVYVCGRTWDDPDYWG 127
DB 68 GRIT-TSGSTNNPBLKSRVMSVDTSKNQPSLKSSVTAADTAYVYCARGRFTYFDYWG 126
QY 128 OGTTLVVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPEPVYVSWNSGALTSGVH 187
DB 127 OGTLVTVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPEPVYVSWNSGALTSGVH 186
QY 188 TEPALVQSSGLYSLSVTVVPPSSNFGTQYTCNVNDHKRPENTVDKTVKCKCVC---CP 244
DB 187 TEPALVQSSGLYSLSVTVVPPSSNFGTQYTCNVNDHKRPENTVDKTVKCKCVC---CP 246
QY 245 CPAPV-VAGPSVFLPPPKKDTLMTSRTPVTCVVDVSHEDPEVQFNMYVDGVEVHNAK 303
DB 247 CPAPV-LGGPSVFLPPPKKDTLMTSRTPVTCVVDVSHEDPEVQFNMYVDGVEVHNAK 306
QY 304 TKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISKYTGQPREPV 363
DB 307 TKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISKYTGQPREPV 366
QY 364 YTLPSREEMTKNOVSLTCLVKGFPYPSDIAVEMNSGQPENNYKTPPMLDSDSPFLYS 423
DB 367 YTLPSREEMTKNOVSLTCLVKGFPYPSDIAVEMNSGQPENNYKTPPMLDSDSPFLYS 426
QY 424 KLTVDKSRWQGNVSCSVMEHALNHNHYTKSLSPGK 462
DB 427 KLTVDKSRWQGNVSCSVMEHALNHNHYTKSLSPGK 465

RESULT 11
Q569F4 HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.

AC Q569F4;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshynski S., Carrincci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51258 MW; AC13448E3047784F CRC64;

Query Match 77.2%; Score 1922.5; DB 2; Length 469;
Best Local Similarity 77.4%; Pred. No. 1.3e-125;
Matches 364; Conservative 41; Mismatches 56; Indels 9; Gaps 4;

QY 1 MECSVLMFLISGTAGVLSVVOLOSGPELVKPGASVWMSCKASGYGTIDYIHMKQSH 60
DB 1 MEFGLSWFVIALKGVQCEVQVYVSSGCVVQPGSLSLSCAAGFTTDDVAMHVQAP 60
QY 61 GKSLEWIGIYVNNNGNGYNOQFKGKATLVVKSSTAYMEIRLTLSSEDAVYVCGRTWDDPDYWG 127
DB 61 GKSLEWIGIYVNNNGNGYNOQFKGKATLVVKSSTAYMEIRLTLSSEDAVYVCGRTWDDPDYWG 126
QY 117 RSTWDDPDYWGOGTTLVVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPEPVYVSWNSGALTSGVH 187
DB 121 YST-AGFYVQGTIVTVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPEPVYVSWNSGALTSGVH 186
QY 177 WNSGALTSGVHTFPVAVLOSGGLYSLSVTVVPPSSNFGTQYTCNVNDHKRPENTVDKTVKCKCVC---CP 244
DB 180 WNSGALTSGVHTFPVAVLOSGGLYSLSVTVVPPSSNFGTQYTCNVNDHKRPENTVDKTVKCKCVC---CP 246
QY 237 KCVCV---CPCPAPV-VAGPSVFLPPPKKDTLMTSRTPVTCVVDVSHEDPEVQFNMYVDGVEVHNAK 303
DB 240 KSCDTHKCPCPAPV-LGGPSVFLPPPKKDTLMTSRTPVTCVVDVSHEDPEVQFNMYVDGVEVHNAK 306
QY 293 YVDGVEVHNAKTKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISKYTGQPREPV 363
DB 300 YVDGVEVHNAKTKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISKYTGQPREPV 366
QY 353 KTKGQPREPVYTLPPSREEMTKNOVSLTCLVKGFPYPSDIAVEMNSGQPENNYKTPPMLDSDSPFLYS 423
DB 427 KTKGQPREPVYTLPPSREEMTKNOVSLTCLVKGFPYPSDIAVEMNSGQPENNYKTPPMLDSDSPFLYS 426

Db 360 KAKQPREPVYTLPPSRDELTKNOVSLTCLVKGFPYDIAVENESNQPERNNKTTTPV 419

Qy 413 LDDSGSFLLYSKLTVDKSRMOQGNFSCVMHEALHNHTYTKSLSLSPGK 462

Db 420 LDDSGSFLLYSKLTVDKSRMOQGNFSCVMHEALHNHTYTKSLSLSPGK 469

RESULTS 12	
06N089 HUMAN	
ID	Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC	Q6N089;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE	Hypothetical protein DKFZp666P15220.
GN	Name=DKFZp666P15220;
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Hominda
OC	Homio.
NCBI	TaxID=9606;

Query Match	77.2%	Score 1922;	DB 2;	Length 472;
Best Local Similarity	76.7%	Pred. No. 1.4e-125;		
Matches 362; Conservative	41;	Mismatches 59;	Indels 10;	Gaps 3

[illegible]

Db	361	ISAKQOPREPOVITILPERKDELITKQVSLTCLVKGFPSPSIAVEMSNQGPENNYHTTP	420
Oy	411	PMUSDGSEFLYSKLTVDKSRMQGQNVFSCSVMHEALHNHTOKSLSPK	462
Db	421	PVLDGSGSEFLYSKLTVDKSRMQGQNVFSCSVMHEALHNHTOKSLSPK	472

RESULT	13
OSR017	PONPY
ID	QSER17_PONPY PRELIMINARY;
AC	QSER17;
DT	01-FEB-2005 (TREMBlrel. 29, Created)
DT	01-FEB-2005 (TREMBlrel. 29, last sequence update)
DT	01-FEB-2005 (TREMBlrel. 29, last annotation update)
DE	Hypotheetical protein DKFZp469C335.
GN	DKFZp469C335;
OS	Pongo pygmaeus (Orangutan).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae
OC	Pongo.
NCBI	TaxID=3600;

Query Match	76.7%	Score 1910.5	DB 2	Length 475
Best Local Similarity	77.0%	Pred. No. 8.8e-125		
Matches 361	Conservative 35	Mismatches 60	Indels 13	Gaps 3

```

QY      7 MLFLTSLGTAUJLSTVUOLQSGBELVTKPPASVYMSCKKASGYGTQDVIYHMKXSHGSLKM 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      7 LALLAVIQAACADILQVQSGAEVARKPBESLILSCGSGCYITTDWIGNRVMPKGLBL 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      67 IGYIYPNNGNGYNOKFKPKATLTVDKSSSTAAMELRTLTSEDSAYVYCGRSRTMD- 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      67 KGMIDPSNSGKYKNSFEGHITISADMISITAYLTQMTISKABDASAIYYCARLISGTNSY 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      123 -----FDVWGGGTTLTVSASTKGSVPIAPCSSTSTSTALGLVNDYEPPEPTVSM 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      127 HKRSTYFQWGGGTTLTVSLASTKGSVPEPLAPSSSTSGTALGLVNDYEPPEPTVSM 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      178 NSGALITSGVHFPAVLQSSGLYLSLSSVYTPSSNSGTQTYTCNVDHKPSNTIYDKTVRK 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      187 NSGALITSGVHFPAVLQSSGLYLSLSSVYTPSSISGTQYICNVDHKPSNTIYDKTVRK 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      238 CC---VEPCPPAP-VAQPSVFLEPPPKDTLMSRPEYTCVVDVSHHEBPQFNNY 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      247 SCDTPRPPCPAPAPLQGPSVFLEPPPKDTLMSRPEYTCVVDVSHHEBPQFNNY 306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      294 VDGVEVNHAKTKPREQGFNSTFRVVSVLTIVHQDMLNGKCYKCVSNKGLPAPIEKTIIR 353

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Db 307 VDGVENHAKTKPREEQNSITFRVSVYLAHVQDMLNGKXCKVSNKALPAPIEKTISK 366
 Qy 354 TKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPM 413
 Db 367 AKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPM 426
 Qy 414 DSDGSFFLYSKLTVDKSRMOQGNVSCSVMEALNHNHYTKSLSPGK 462
 Db 427 DSDGSFFLYSKLTVDKSRMOQGNVSCSVMEALNHNHYTKSLSPGK 475
 RESULT 14
 O6PJ44 HUMAN PRELIMINARY; PRT; 470 AA.
 ID O6PJ44_HUMAN PRELIMINARY; PRT; 470 AA.
 AC O6PJ44_HUMAN PRELIMINARY; PRT; 470 AA.
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raba S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Scherch A., Schein J.E., Jones S.J.M., Skalska U., Smalhus D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC018747; AAH18747.1; -, mRNA.
 DR HSP; F01861; IADQ.
 DR SMR; Q6PJ44; 20-470.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC UNKNOW; 2.
 DR PROSITE; PS00290; IG_MHC UNKNOW; 2.
 SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Matches 361; Conservative 43; Mismatches 58; Indels 8; Gaps 4;
 Qy 1 MECSVMFLISGTAAGVSEVOLQOSGEIKRPGASVMSKASGYGTGYTHMKOSH 60
 Db 1 MELGISWFLVAILGEVCEVQLVESGGGLVQPGSLKSCVSGFTISSTMSVNRQAP 60
 Qy 61 GKSLEWIGIYIPNNNGNGYNKFKGKATLTVDKSSSTAYMELRTLSEDSAVYYGR--S 118
 Db 61 GKGLEWVNIQDQSEKTYVSVKGRFTISDNANGLSLYLQNSLRADDTAYVCARDSS 120
 Qy 119 TW--DDPDYWGQTTLVYSASTKSPVPLAPCSRSTSESTALGCLVKDYPPRPVYS 176
 Db 121 SWYRDWFPWCGITLVVTSASTKSPVPLAPSSKSTSGTALGCLVKDYPPRPVYS 180
 Qy 177 WNSGALTSVHTFPFVAVLQSSGLYSLSVVTVPSSAFGQTQVNDHPSNKKVQTVYR 236
 Db 181 WNSGALTSVHTFPFVAVLQSSGLYSLSVVTVPSSAFGQTQVYICVNNHPSNKKVQTVYR 240
 Qy 237 KCVE---CPPCPAPP-VAGPSVFLPPPKPDTLMISRTPEVTVVVDVSHEDPEVQFM 292
 Db 241 KSCDKTHCPCCPAPPELLGSPVFLPPPKPDTLMISRTPEVTVVVDVSHEDPEVQFM 300
 Qy 293 YDGVENHAKTKPREEQNSITFRVSVYLAHVQDMLNGKXCKVSNKALPAPIEKTIS 352
 Db 301 YDGVENHAKTKPREEQNSITFRVSVYLAHVQDMLNGKXCKVSNKALPAPIEKTIS 360
 Qy 353 KTKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPM 412
 Db 361 KAKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIAVEMSNQGPENNYKTTTPM 420
 Qy 413 LDSDGSFFLYSKLTVDKSRMOQGNVSCSVMEALNHNHYTKSLSPGK 462
 Db 421 LDSDGSFFLYSKLTVDKSRMOQGNVSCSVMEALNHNHYTKSLSPGK 470
 RESULT 15
 O6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
 ID O6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
 AC O6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raba S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Scherch A., Schein J.E., Jones S.J.M., Skalska U., Smalhus D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]

Query Match 76.7%; Score 1909; DB 2; Length 470;
 Best Local Similarity 76.8%; Pred. No. 1.1e-124;

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073773; AA73773.1; -; mRNA.
 DR GO; GO:0016021; C:intrigal to membrane; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-11ke.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_Y.
 DR Pfam; PF07654; C1-sec; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 76.5%; Score 1904; DB 2; Length 476;
 Best Local Similarity 76.8%; Pred. No. 2, 5e-124;

Matches 361; Conservative 41; Mismatches 52; Indels 16; Gaps 6;

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QY      8 LFLSGTAGVISEVOIQSGPELVKPGASVKNMCKASG--YTGTDYYIHMKQSHGKSLE 65
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 67
QY      66 WIGYIYNNNGGNGVYNGKFKGKATLTVDKSSSTAYMELRTLSBDSAVYCGRS----- 118
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 126
QY      68 WIGYIY-YSGSTYNNLSKRVYISLDTKNOFSLKNSVTADTAIVPCARAGWGGR 126
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 186
QY      119 TW--DQFDYWGQGTTLTVSSASTKGPSVEPLAPCSRSTSESTALGCLVKDYFPEPVTVS 176
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 186
QY      127 SWAIDGFNIMWGCTMTVTSASSTKGPSVFPLAPSSKSTSGTALAQLVNDYFPEPVTVS 186
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 236
QY      177 WNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVR 236
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 246
QY      187 WNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVNHKPSNTKVDKTVR 246
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 292
QY      237 KCCVE---GPPCPAPP-VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNV 292
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 306
QY      247 KSCDKHTHTCPCPAPPELGGPSVFLEPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNV 306
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 352
QY      293 YVDGYEVHNAKTPREEQNSTFRVYSVLTVVHQMVLNGKEYKCKVSNKGLPAPIEKTI 352
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 366
QY      307 YVDGYEVHNAKTPREEQNSTFRVYSVLTVVHQMVLNGKEYKCKVSNKGLPAPIEKTI 366
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 412
QY      353 KTKGQPREPQVYTLTPSRSEMTKNQVSLTCLVKGYFPSDIAVWESNNGQPENNYKTTTPM 412
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 426
QY      367 KAKGQPREPQVYTLTPSRDELFTNQVSLTCLVKGYFPSDIAVWESNNGQPENNYKTTTPV 426
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 462
QY      413 LPSDGSFELYSLTLDKSRWQGNVSCVMHEALHNHYTQKSLSLSPGK 462
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 476
QY      427 LPSDGSFELYSLTLDKSRWQGNVSCVMHEALHNHYTQKSLSLSPGK 476
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Search completed: January 24, 2006, 18:56:20
 Job time : 152.695 secs

QY 317 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 376
DB 301 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 360
QY 377 QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRMOQGN 436
DB 361 QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRMOQGN 420
QY 437 VFSCSVMEBALHNNHTYOKSLSLSPGK 462
DB 421 VFSCSVMEBALHNNHTYOKSLSLSPGK 446

RESULT 2
US-11-102-621-126
; Sequence 126, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-126

Query Match 86.1%; Score 2143.5; DB 7; Length 442;
Best Local Similarity 90.1%; Pred. No. 1.4e-131;
Matches 399; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

QY 20 EVLOQSGPELVKPGASVYKSCASGYGTDTYIHHMKQSHGKSLWIGIYIPNNNGNGY 79
DB 1 QVQLVQSGAEVKKPKASVYKSCASGYFTSYRMHWVQAPOGLWMIGIYINPSGYTEY 60
QY 80 NQKFKGKATLTVDKSSSTAYMELRTLTSEDAVYTCGRSTMDPDTWGGTTLTVSSAST 139
DB 61 NQKFKDKATLTADSESTINAYMELSLRSEDTAVYTCARG-GGVFDYWGQGLTVTVSSAST 119
QY 140 KQPSVFPLAPCSRSTSESTALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSSGLY 199
DB 120 KQPSVFPLAPCSRSTSESTALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSSGLY 179
QY 200 SLSSVTVVSSNFGITQYTCNVDPKPSNTKVDKVERKCCVCEPCPAPPAAPVAPSVFLFP 259
DB 180 SLSSVTVVSSNFGITQYTCNVDPKPSNTKVDKVERKCCVCEPCPAPPAAPVAPSVFLFP 239
QY 260 PRPKDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFRVVS 319
DB 240 PRPKDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFRVVS 299
QY 320 VLTIVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKNQVS 379
DB 300 VLTIVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKNQVS 359
QY 380 LITCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRMOQGNVVS 439
DB 360 LITCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRMOQGNVVS 419
QY 440 CSVMHEBALHNNHTYOKSLSLSPGK 462
DB 421 CSVMHEBALHNNHTYOKSLSLSPGK 446

DB 420 CSVMHEBALHNNHTYOKSLSLSPGK 442

RESULT 3
US-11-102-621-136
; Sequence 136, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-136

Query Match 86.0%; Score 2142.5; DB 7; Length 446;
Best Local Similarity 89.7%; Pred. No. 1.7e-131;
Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1;

QY 20 EVLOQSGPELVKPGASVYKSCASGYGTDTYIHHMKQSHGKSLWIGIYIPNNNGNGY 79
DB 1 QVQLVQSGAEVKKPKASVYKSCASGYFTSYRMHWVQAPOGLWMIGIYINPSGYTEY 60
QY 80 NQKFKGKATLTVDKSSSTAYMELRTLTSEDAVYTCGRSTMDPDTWGGTTLTVSSAST 136
DB 61 NQKFKDKATLTADSESTINAYMELSLRSEDTAVYTCARGAAYDYDGFAYWGQGLTVTVSS 120
QY 137 ASTKQPSVFPLAPCSRSTSESTALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSS 196
DB 121 ASTKQPSVFPLAPCSRSTSESTALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSS 180
QY 197 GLYSLSVTVVSSNFGITQYTCNVDPKPSNTKVDKVERKCCVCEPCPAPPAAPVAPSVF 256
DB 181 GLYSLSVTVVSSNFGITQYTCNVDPKPSNTKVDKVERKCCVCEPCPAPPAAPVAPSVF 240
QY 257 LPPPKQDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFR 316
DB 241 LPPPKQDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFR 300
QY 317 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 376
DB 301 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 360
QY 377 QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRMOQGN 436
DB 361 QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRMOQGN 420
QY 437 VFSCSVMEBALHNNHTYOKSLSLSPGK 462
DB 421 VFSCSVMEBALHNNHTYOKSLSLSPGK 446

RESULT 4
US-11-102-621-137
; Sequence 137, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya

APPLICANT: Tso, J. Yun
APPLICANT: Vasequez, Maximiliano
TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US 10/822,300
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-11-102-621-137

Query Match 86.0%; Score 2142.5; DB 7; Length 446;
Best Local Similarity 89.7%; Pred. No. 1.7e-131;
Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1;

QY 20 EVQLQDSPELVKPKASVYKSCASGYTGTDTYTHMMQSHGKSLKEMIGIYIPNNGNGY 79
DB 1 QVQLVQSGAEYKPKASVYKSCASGYTFTSYTHMMVWQAPQGQLEMMGYINPSGYTHY 60
QY 80 NQKFKGKATLVNDSKSSATYAMELRTITSEDSAVYVCGSTWDDPD---YMGQGTLLTVSS 136
DB 61 NQKFKGKATLVNDSKSSATYAMELRTITSEDSAVYVCGSTWDDPD---YMGQGTLLTVSS 120
QY 137 ASTGKPSVFLAPCSRSTSESTALGCLVNDYFPEPVTVSNNSGALTSGVHTFPVAVLQSS 196
DB 121 ASTGKPSVFLAPCSRSTSESTALGCLVNDYFPEPVTVSNNSGALTSGVHTFPVAVLQSS 180
QY 197 GLYSLSVYTPSSNFGTQYTCVNDHKPSNTKVDKTYERKCCVCEPCPAPPAAGPSVFLP 256
DB 181 GLYSLSVYTPSSNFGTQYTCVNDHKPSNTKVDKTYERKCCVCEPCPAPPAAGPSVFLP 240
QY 257 LPPPKDQTLMIISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVNAKTKPREBOFNSTFRV 316
DB 241 LPPPKDQTLMIISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVNAKTKPREBOFNSTFRV 300
QY 317 VSVTLVTHQDMNGKCYKCKVSNKGLPAPIEKTISKTKGQPREQVYTLTPSRREEMTKN 376
DB 301 VSVTLVTHQDMNGKCYKCKVSNKGLPAPIEKTISKTKGQPREQVYTLTPSRREEMTKN 360
QY 377 QVSLTCLVKGFPSPDIAYEWESNQPENNYKTPPMLDSDGSFPLYSKLTVDKSRWQGN 436
DB 361 QVSLTCLVKGFPSPDIAYEWESNQPENNYKTPPMLDSDGSFPLYSKLTVDKSRWQGN 420
QY 437 VFCSCVMHEALHNHTYOKSLSLSPGK 462
DB 421 VFCSCVMHEALHNHTYOKSLSLSPGK 446

RESULT 5
US-11-102-621-124

Sequence 124, Application US/11102621
Publication No. US20050276799A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R.
APPLICANT: Tsurushita, Naoya
APPLICANT: Tso, J. Yun
APPLICANT: Vasequez, Maximiliano
TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US 10/822,300
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2

SEQ ID NO 124
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-11-102-621-124

Query Match 86.0%; Score 2140.5; DB 7; Length 442;
Best Local Similarity 90.1%; Pred. No. 2.2e-131;
Matches 399; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 20 EVQLQDSPELVKPKASVYKSCASGYTGTDTYTHMMQSHGKSLKEMIGIYIPNNGNGY 79
DB 1 QVQLVQSGAEYKPKASVYKSCASGYTFTSYTHMMVWQAPQGQLEMMGYINPSGYTHY 60
QY 80 NQKFKGKATLVNDSKSSATYAMELRTITSEDSAVYVCGSTWDDPDYMGQGTLLTVSSAST 139
DB 61 NQKFKGKATLVNDSKSSATYAMELRTITSEDSAVYVCGSTWDDPDYMGQGTLLTVSSAST 119
QY 140 KGPSVFLAPCSRSTSESTALGCLVNDYFPEPVTVSNNSGALTSGVHTFPVAVLQSSGLY 199
DB 120 KGPSVFLAPCSRSTSESTALGCLVNDYFPEPVTVSNNSGALTSGVHTFPVAVLQSSGLY 179
QY 200 SLSSVYTPSSNFGTQYTCVNDHKPSNTKVDKTYERKCCVCEPCPAPPAAGPSVFLP 259
DB 180 SLSSVYTPSSNFGTQYTCVNDHKPSNTKVDKTYERKCCVCEPCPAPPAAGPSVFLP 239
QY 260 PKPKDQTLMIISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVNAKTKPREBOFNSTFRV 319
DB 240 PKPKDQTLMIISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVNAKTKPREBOFNSTFRV 299
QY 320 VLTIVHQMNGKCYKCKVSNKGLPAPIEKTISKTKGQPREQVYTLTPSRREEMTKN 379
DB 300 VLTIVHQMNGKCYKCKVSNKGLPAPIEKTISKTKGQPREQVYTLTPSRREEMTKN 359
QY 380 LTLVKGFPSPDIAYEWESNQPENNYKTPPMLDSDGSFPLYSKLTVDKSRWQGNVFS 439
DB 360 LTLVKGFPSPDIAYEWESNQPENNYKTPPMLDSDGSFPLYSKLTVDKSRWQGNVFS 419
QY 440 CSVMHEALHNHTYOKSLSLSPGK 462
DB 420 CSVMHEALHNHTYOKSLSLSPGK 442

RESULT 6
US-11-102-621-125

Sequence 125, Application US/11102621
Publication No. US20050276799A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R.
APPLICANT: Tsurushita, Naoya
APPLICANT: Tso, J. Yun
APPLICANT: Vasequez, Maximiliano
TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US 10/822,300
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 125
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-11-102-621-125

Query Match 86.0%; Score 2140.5; DB 7; Length 442;
Best Local Similarity 90.1%; Pred. No. 2.2e-131;
Matches 399; Conservative 17; Mismatches 26; Indels 1; Gaps 1;
QY 20 EVQLQDSPELVKPKASVYKSCASGYTGTDTYTHMMQSHGKSLKEMIGIYIPNNGNGY 79

```

Db      1  QVQLVQSGAEVKKPKSSSKAGGYTFTSYRMHVRQAPQGLEWIGYINPSTGYTEY 60
Qy      80  NQKFKGKATLTVDKSSSTAYMELRTLSBDSAVYVCGASITMDDFDYMGQGITLTIVSSAST 139
        61  NQKFKDKATITIDESTINRAYMELSLRSBETAVYVCGAG-GGVFTYMGQGITLVYSSAST 119
Qy      140  KGPSVFPLAAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 199
        120  KGPSVFPLAAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 179
Qy      200  SLSSVTVTPSSNFGQTYTCNVDHPSNTKVDKTERKCCVCPCPAPPAAPAVSVFLFP 259
        180  SLSSVTVTPSSNFGQTYTCNVDHPSNTKVDKTERKCCVCPCPAPPAAPAVSVFLFP 239
Qy      260  PKPKDTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 319
        240  PKPKDTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 299
Qy      320  VLTAVHQMVLNKEKCYKCVSNKGLPAPLEKTI SKTKGQPREPOVYTLPPSRREMTKNQVS 379
        300  VLTAVHQMVLNKEKCYKCVSNKGLPAPLEKTI SKTKGQPREPOVYTLPPSRREMTKNQVS 359
Qy      380  LTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSGFFLYSKLTVDKSRMWOQGNVFS 439
        360  LTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSGFFLYSKLTVDKSRMWOQGNVFS 419
Qy      440  CSVMHEALHNHYTOKSLSLSPCK 462
        420  CSVMHEALHNHYTOKSLSLSPCK 442

```

RESULT 7

```

US-11-102-621-139
; Sequence 139, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Taurushita, Naoya
; APPLICANT: Teo, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-139

```

Query Match 85.9%; Score 2139.5; DB 7; Length 446;

Best Local Similarity 89.5%; Pred. No. 2,6e-131;

Matches 399; Conservative 17; Mismatches 27; Indels 3; Gaps 1;

```

Qy      20  EVQLQDSGPELVKPGASVYMSCKASGYTGTIDYIHMNKQSHGKSLDWIGIYIPNNGNGY 79
        1  QVQLVQSGAEVKKPKSSSKAGGYTFTSYRMHVRQAPQGLEWIGYINPSTGYTEY 60
Qy      80  NQKFKGKATLTVDKSSSTAYMELRTLSBDSAVYVCGASITMDDFDYMGQGITLTIVSSAST 136
        61  NQKFKDKATITIDESTINRAYMELSLRSBETAVYVCGAG-GGVFTYMGQGITLVYSSAST 120
Qy      120  ASTKGPSVFPLAAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 196
        121  ASTKGPSVFPLAAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 180

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Qy      197  GLYSLSVTVTPSSNFGQTYTCNVDHPSNTKVDKTERKCCVCPCPAPPAAPAVSVFLFP 256
        181  GLYSLSVTVTPSSNFGQTYTCNVDHPSNTKVDKTERKCCVCPCPAPPAAPAVSVFLFP 240
Qy      257  LPPPKDTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFR 316
        241  LPPPKDTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFR 300
Qy      317  VVSVLTAVHQMVLNKEKCYKCVSNKGLPAPLEKTI SKTKGQPREPOVYTLPPSRREMTKN 376
        301  VVSVLTAVHQMVLNKEKCYKCVSNKGLPAPLEKTI SKTKGQPREPOVYTLPPSRREMTKN 360
Qy      377  QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSGFFLYSKLTVDKSRMWOQGN 436
        361  QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPMLDSGFFLYSKLTVDKSRMWOQGN 420
Qy      437  VFSCSVMEALHNHYTOKSLSLSPCK 462
        421  VFSCSVMEALHNHYTOKSLSLSPCK 446

```

RESULT 8

```

US-11-102-621-127
; Sequence 127, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Taurushita, Naoya
; APPLICANT: Teo, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 127
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-127

```

Query Match 85.8%; Score 2137.5; DB 7; Length 442;

Best Local Similarity 89.8%; Pred. No. 3.4e-131;

Matches 398; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

```

Qy      20  EVQLQDSGPELVKPGASVYMSCKASGYTGTIDYIHMNKQSHGKSLDWIGIYIPNNGNGY 79
        1  QVQLVQSGAEVKKPKSSSKAGGYTFTSYRMHVRQAPQGLEWIGYINPSTGYTEY 60
Qy      80  NQKFKGKATLTVDKSSSTAYMELRTLSBDSAVYVCGASITMDDFDYMGQGITLTIVSSAST 139
        61  NQKFKDKATITIDESTINRAYMELSLRSBETAVYVCGAG-GGVFTYMGQGITLVYSSAST 119
Qy      140  KGPSVFPLAAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 199
        120  KGPSVFPLAAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 179
Qy      200  SLSSVTVTPSSNFGQTYTCNVDHPSNTKVDKTERKCCVCPCPAPPAAPAVSVFLFP 259
        180  SLSSVTVTPSSNFGQTYTCNVDHPSNTKVDKTERKCCVCPCPAPPAAPAVSVFLFP 239
Qy      260  PKPKDTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 319
        240  PKPKDTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 299
Qy      320  VLTAVHQMVLNKEKCYKCVSNKGLPAPLEKTI SKTKGQPREPOVYTLPPSRREMTKNQVS 379
        300  VLTAVHQMVLNKEKCYKCVSNKGLPAPLEKTI SKTKGQPREPOVYTLPPSRREMTKNQVS 359

```

Qy	Db	Qy	Db
380	ITCLVKGFPSPSIAVEMESNGCPENNYYKTTPTMLDSDGSFLYSKLTVPKSRMGOQNVFS	440	CSVMEHALNNHTTOKSLSPGK 462
360	LITCLVKGFPSPSIAVEMESNGCPENNYYKTTPTMLDSDGSFLYSKLTVPKSRMGOQNVFS	420	CSVLTEALNNHTOKSLSPGK 442

RESULT 9	;	TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
US-11-102-621-140	;	FILE REFERENCE: 05882.0039.00PC03

```

: Sequence 140, Application US/11102621
: Publication No. US20050276799A1
: GENERAL INFORMATION:
: APPLICANT: Protein Design Labs, Inc.
: APPLICANT: Hinton, Paul R.
: APPLICANT: Tsurushita, Naoya
: APPLICANT: Tso, J. Yun
: APPLICANT: Vasquez, Maximiliano
: TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
: TITLE OF INVENTION: ANTIBODIES FOR MTOXAGENESIS
: FILE REFERENCE: 05882.0039.00PC03
: CURRENT APPLICATION NUMBER: US/11/102,621
: CURRENT FILING DATE: 2005-04-08
: PRIOR APPLICATION NUMBER: US 10/822,300
: PRIOR FILING DATE: 2004-04-09
: NUMBER OF SEQ ID NOS: 146
: SOFTWARE: Patentin version 3.2
: SEQ ID NO 140
: LENGTH: 446
: TYPE: prt
: ORGANISM: Homo sapiens
: US-11-102-621-140

```

Query Match	85.8%	Score 2137.5	DB 7	Length 446
Best Local Similarity	89.5%	Pred. No. 3.5e-131		
Matches 399, Conservative	16	Mismatches 28	Indels 3	Gaps 1

```

QY 20 EYUOLQOOSGEYLKPGASVYMSCKASGYTGDDYIHHMKOSHGSLEIGIYVNNQNGY 79
Db 1 QVULVQSGAEVKKPGASVYVSCASASYYTITSTMHWVRQAPGGGLEMGYINRSGTTH 60
QY 80 NQKPYGKATLVYDKSSSTAYMEIRLTLSBDASAYYCGRSTWDFD--YWGQSTLLTVSS 136
Db 61 NQKLDKATLVADKASASTAYMEILSSRSEDATYYCARASAYYDDGPAYWGGQGLTVSS 120
QY 137 ASTKGPVYPLAPCSASTSESTAAAGCYKDYRPEPYTYSWNSGALTSCHTTPAYLQSS 196
Db 121 ASTKGPVYPLAPCSASTSESTAAAGCYKDYRPEPYTYSWNSGALTSCHTTPAYLQSS 180
QY 197 GLYSLSVTVYVSSNNGTQTYTGNVDHKSNSTLYDKTVERRKCCVCECPCAPAPVAGSVF 256
Db 181 GLYSLSVTVYVSSNNGTQTYTGNVDHKSNSTLYDKTVERRKCCVCECPCAPAPVAGSVF 240
QY 257 LFPKPKDTLMTSRPEVTCCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKRBEQFNSTFR 316
Db 241 LFPKPKQDTLMTSRPEVTCCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKRBEQFNSTFR 300
QY 317 VVSVLTVYHQMNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOYYTLPPRSREEMTKN 376
Db 301 VVSVLTVYHQMNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOYYTLPPRSREEMTKN 360
QY 377 QVSLTCLVKGFPYPSDIAVWESNQGQDENNYKTPPMLDSDGSFFLYSKLTVDKSRWQGN 436
Db 361 QVSLTCLVKGFPYPSDIAVWESNQGQDENNYKTPPMLDSDGSFFLYSKLTVDKSRWQGN 420
QY 437 VFGCSVMHEALNNHYTKSLSPRK 462
Db 421 VFGCSVMHEALNNHYTKSLSPRK 446

```

RESULT 10

```

US-11-102-621128
; Sequence 128, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882, 0039, 00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 128
; LENGTH: 442
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-102-621128

```

Query Match	85.8%;	Score 2135.5;	DB 7;	Length 442;
Best Local Similarity	89.8%;	Pred. No. 4.6e-131;		
Matches 398;	Conservative 17;	Mismatches 27;	Indels 1;	Gaps 1

QY	20	EYVLQLOOSPBLVTPKPAASYVMCKASGYCTDYYHHMKOSHGLSEIMIGIYVNNNGNGY	79
Db	1	QVQLVQSGAEVKKVPPSSVAVKSCASGYITFTSRMHVWROAPGGGLEIMIGIYNPSTGTTEY	60
QY	80	NOFKFKGAKTLTVYDKSSSTAYMEILTLTSEDSAVYVYCGSRSTWDDFDYMGQGITLVLSASAST	139
Db	61	NOKFKDQAKITITADESTNTAYMELSLRSBEDTAIVYVCARG- GGVEFDYMGQGITLVLSASAST	119
QY	140	KGPSVFPLAPCRSTSTSESTALAGCLVKDYFPEPVYVYVSNMSGALTSGVHTFPAPALQSSGLY	199
Db	130	KGPSVFPLAPCRSTSTSESTALAGCLVKDYFPEPVYVYVSNMSGALTSGVHTFPAPALQSSGLY	179
QY	200	SLSSVYVTPSSNPFQGYTYTCNDVHKPSNKKVDTKYERKCKVCECPCPAPRVAPGPSVFLFP	258
Db	180	SLSSVYVTPSSNPFQGYTYTCNDVHKPSNKKVDTKYERKCKVCECPCPAPRVAPGPSVFLFP	239
QY	260	PKPKDTLMISRTPEVYTCVVDVSHEDPEVQFNMYVDVGEVHNNAKTKPRBEQFNSTPRVVS	319
Db	240	PKPKDQLMISRPEVYTCVVDVSHEDPEVQFNMYVDVGEVHNNAKTKPRBEQFNSTPRVVS	299
QY	320	VLTVNHODMLNKEKVKCKVSNKGFLPARIKTKTSTKGGQRPBPQVYTLPRPREEMTKNOVS	379
Db	300	VLTVNHODMLNKEKVKCKVSNKGFLPARIKTKTSTKGGQRPBPQVYTLPRPREEMTKNOVS	359
QY	380	LTCLVKGFFYPSDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRKQOQGNVFS	439
Db	360	LTCLVKGFFYPSDIAVEMESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRKQOQGNVFS	419
QY	440	CSVMEHALNHNHTOKSLSPGK 462	
Db	420	CSVFHEALNHNHTOKSLSPGK 442	

RESULT 11

US-11-025-712-12
; Sequence 12, Application US/11025712
; Publication No. US20050255108A1

GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
Thomas, G. Roger
Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3
CURRENT APPLICATION NUMBER: US/11/128,900
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/776649
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 10/612497
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 2003-07-01
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113647
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-2

Query Match 83.4%; Score 2076; DB 7; Length 464;
Best Local Similarity 83.2%; Pred. No. 3.3e-127;
Matches 386; Conservative 31; Mismatches 45; Indels 2; Gaps 1;

QY 1 MECSGWMFLSSTAGVLSVQLQSGPELVKPGASVMSCKASGYGTDYIHHMKQSH 60
DB 1 MEFGLSWFLVALLRGVQCVQLVESGGGVQPGSLRLSTASGFTSNMGHWVRQAP 60
QY 61 GKSLEWIGYIYPNNGNGYNGKFKGKATLVTKSSSTAYMELRTLTSEDAVYYC--GRS 118
DB 61 GKGLEWAVAVIYDSGNKHGYSVKRFTISSDNGNTLYLQNSLRADTAIVYICARER 120
QY 119 TWDFDVGQGTTLTVSSASATKGPSVPLAPCSSTSTSTALGCLVNDYPEPYVSMN 178
DB 121 LGSYFDVYGQGTTLTVSSASATKGPSVPLAPCSSTSTSTALGCLVNDYPEPYVSMN 180
QY 179 SGALTSGVHTPVAIVQSSGLYSLSVTVPSNFGTQTYTCNVHDKPSNTKYDKTVERKC 238
DB 181 SGALTSGVHTPVAIVQSSGLYSLSVTVPSNFGTQTYTCNVHDKPSNTKYDKTVERKC 240
QY 239 CVECPPCAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQPMYVDGE 298
DB 241 CVECPPCAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQPMYVDGE 300
QY 299 VHNATKREBQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIEKTISTKQCP 358
DB 301 VHNATKREBQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIEKTISTKQCP 360
QY 359 REPQVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPMLDSGS 418
DB 361 REPQVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPMLDSGS 420
QY 419 FFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 462
DB 421 FFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 464

RESULT 14
US-11-128-900-66
Sequence 66, Application US/11128900
Publication No. US20050287136A1
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEORFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3
CURRENT APPLICATION NUMBER: US/11/128,900

CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/776649
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 10/612497
PRIOR FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 09/472087
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113647
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-66

Query Match 83.4%; Score 2076; DB 7; Length 464;
Best Local Similarity 83.2%; Pred. No. 3.3e-127;
Matches 386; Conservative 31; Mismatches 45; Indels 2; Gaps 1;

QY 1 MECSGWMFLSSTAGVLSVQLQSGPELVKPGASVMSCKASGYGTDYIHHMKQSH 60
DB 1 MEFGLSWFLVALLRGVQCVQLVESGGGVQPGSLRLSTASGFTSNMGHWVRQAP 60
QY 61 GKSLEWIGYIYPNNGNGYNGKFKGKATLVTKSSSTAYMELRTLTSEDAVYYC--GRS 118
DB 61 GKGLEWAVAVIYDSGNKHGYSVKRFTISSDNGNTLYLQNSLRADTAIVYICARER 120
QY 119 TWDFDVGQGTTLTVSSASATKGPSVPLAPCSSTSTSTALGCLVNDYPEPYVSMN 178
DB 121 LGSYFDVYGQGTTLTVSSASATKGPSVPLAPCSSTSTSTALGCLVNDYPEPYVSMN 180
QY 179 SGALTSGVHTPVAIVQSSGLYSLSVTVPSNFGTQTYTCNVHDKPSNTKYDKTVERKC 238
DB 181 SGALTSGVHTPVAIVQSSGLYSLSVTVPSNFGTQTYTCNVHDKPSNTKYDKTVERKC 240
QY 239 CVECPPCAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQPMYVDGE 298
DB 241 CVECPPCAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQPMYVDGE 300
QY 299 VHNATKREBQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIEKTISTKQCP 358
DB 301 VHNATKREBQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIEKTISTKQCP 360
QY 359 REPQVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPMLDSGS 418
DB 361 REPQVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPMLDSGS 420
QY 419 FFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 462
DB 421 FFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 464

RESULT 15
US-11-004-590-233
Sequence 233, Application US/11004590
Publication No. US20060008883A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjardais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
FILE REFERENCE: 185832/US/5
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/581,613
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR FILING DATE: 2004-08-13

/ PRIOR APPLICATION NUMBER: US 60/619,483
/ PRIOR FILING DATE: 2004-10-14
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 233
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-11-004-590-233

Query Match 83.3%; Score 2074.5; DB 7; Length 444;
Best Local Similarity 86.5%; Pred. No. 3.9e-127;
Matches 386; Conservative 26; Mismatches 29; Indels 5; Gaps 3;

QY 20 EYQLQSGPELVKPGASVMSCKASGYGTDYIHHMKSHGKSLIEWIGYIPNNGNXY 79
DB 1 QQLVQSGAEVKKPGASVMSCKASGYGTTSTYISWROAPQALMMKMTYAGSGNTKY 60
QY 80 NOKFKGKATLVYDKSSSTAYMEIRLTSDSAVYCGR--STMDDPDYWGQGITLVSSA 137
DB 61 SQKFGGRFVFSYDTSASTAYLQISLKAEDTAVYICANYGNW--FAYWGQGITLVSSA 118
QY 138 STKGSPVFPPLAPCSSTSESTALGCLVQDYFPEPYTWSNGALTSGVHTPPAVLQSSG 197
DB 119 STKGSPVFPPLAPCSSTSESTALGCLVQDYFPEPYTWSNGALTSGVHTPPAVLQSSG 178
QY 198 LYSLSVTVVPSNPGTGTTCNVDHKPSNTKVDKVERKCCVECPCPAPP-VAGPSVF 256
DB 179 LYSLSVTVVPSNPGTGTTCNVDHKPSNTKVDKVERKCCVECPCPAPP-VAGPSVF 238
QY 257 LFPPKPKDTLMI SRTPPEVLCVVVDVSHEDPEVQFMVYVDGVEVHNAKTKPREEQFNSTFR 316
DB 239 LFPPKPKDTLMI SRTPPEVLCVVVDVSHEDPEVQFMVYVDGVEVHNAKTKPREEQFNSTFR 298
QY 317 VTSVLTVHQDWLNGKEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 376
DB 299 VTSVLTVHQDWLNGKEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 358
QY 377 QVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTPPMLDSGSPFLYSKLTVDKSRMOQGN 436
DB 359 QVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTPPMLDSGSPFLYSKLTVDKSRMOQGN 418
QY 437 VFSCSVMEALHNHYTQKSLSLSPGK 462
DB 419 VFSCSVMEALHNHYTQKSLSLSPGK 444

Search completed: January 24, 2006, 19:13:54
Job time : 23.4721 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 24, 2006, 18:56:50 ; Search time 113.021 Seconds
(without alignments)
1707.969 Million cell updates/sec

Title: US-10-828-782A-18

Perfect score: 2490
Sequence: 1 MECSCVMLFLISGTAGVLSLSE.....MHKALHNYTKSLSLSPGK 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2490	100.0	462	US-10-828-782A-18	Sequence 18, Appl
2	2185.5	87.8	461	US-09-249-011A-24	Sequence 24, Appl
3	2174	87.3	470	US-09-859-053-28	Sequence 28, Appl
4	2174	87.3	470	US-10-800-250-28	Sequence 28, Appl
5	2174	87.3	470	US-10-625-105-28	Sequence 28, Appl
6	2172.5	87.2	471	US-10-292-088-46	Sequence 46, Appl
7	2153	86.5	464	US-10-938-353-22	Sequence 22, Appl
8	2146.5	86.2	469	US-10-835-641-23	Sequence 23, Appl
9	2146	86.2	465	US-10-910-901-12	Sequence 2, Appl
10	2145.5	86.2	465	US-10-822-300-138	Sequence 138, Appl
11	2143.5	86.1	442	US-10-822-300-126	Sequence 126, Appl
12	2143.5	86.1	469	US-11-031-485-34	Sequence 34, Appl
13	2144.5	86.0	446	US-10-822-300-136	Sequence 136, Appl
14	2144.5	86.0	446	US-10-822-300-137	Sequence 137, Appl
15	2144.5	86.0	446	US-10-822-300-134	Sequence 124, Appl
16	2140.5	86.0	442	US-10-822-300-125	Sequence 125, Appl
17	2139.5	86.0	446	US-10-822-300-119	Sequence 119, Appl
18	2137.5	85.8	446	US-10-822-300-117	Sequence 117, Appl
19	2137.5	85.8	446	US-11-031-485-42	Sequence 42, Appl
20	2137.5	85.8	446	US-10-822-300-140	Sequence 140, Appl
21	2135.5	85.8	442	US-09-301-593-108	Sequence 128, Appl
22	2128	85.5	472	US-10-159-006-30	Sequence 30, Appl
23	2128	85.5	472	US-10-159-006-30	Sequence 30, Appl
24	2127.5	85.4	461	US-11-034-655-16	Sequence 16, Appl
25	2108	84.7	445	US-10-644-277-38	Sequence 38, Appl
26	2107	84.6	445	US-10-644-277-18	Sequence 18, Appl
27	2105	84.5	445	US-10-644-277-90	Sequence 90, Appl

28	2103.5	84.5	450	US-09-811-384-12	Sequence 12, Appl
29	2103.5	84.5	450	US-10-404-286-12	Sequence 12, Appl
30	2103	84.5	445	US-10-644-277-2	Sequence 2, Appl
31	2089.5	83.9	463	US-10-656-769-34	Sequence 34, Appl
32	2088	83.9	462	US-10-910-901-14	Sequence 14, Appl
33	2086	83.8	468	US-10-723-003-12	Sequence 12, Appl
34	2086	83.8	468	US-11-004-639-12	Sequence 12, Appl
35	2086	83.8	624	US-10-723-003-30	Sequence 30, Appl
36	2086	83.8	624	US-11-004-639-30	Sequence 30, Appl
37	2086	83.8	639	US-10-723-003-32	Sequence 32, Appl
38	2086	83.8	639	US-11-004-639-32	Sequence 32, Appl
39	2084	83.7	470	US-11-019-180-4	Sequence 4, Appl
40	2084	83.7	472	US-10-006-593-67	Sequence 67, Appl
41	2084	83.7	472	US-10-307-724-67	Sequence 67, Appl
42	2084	83.7	472	US-10-737-290-67	Sequence 67, Appl
43	2076	83.4	460	US-10-938-353-26	Sequence 26, Appl
44	2076	83.4	460	US-10-938-353-74	Sequence 74, Appl
45	2076	83.4	464	US-10-153-382-9	Sequence 9, Appl

ALIGNMENTS

```

RESULT 1
US-10-828-782A-18
; Sequence 18, Application US/10828782A
; Publication No. US20040242848A1
; GENERAL INFORMATION:
; APPLICANT: Owens, S. Michael.
; TITLE OF INVENTION: Mouse/Human Chimeric Anti-Phencyclidine
; TITLE OF INVENTION: Antibody And Uses Thereof
; FILE REFERENCE: D6508
; CURRENT APPLICATION NUMBER: US/10/828,782A
; PRIOR FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US/99/046,190
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 18
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of anti-PCP
; OTHER INFORMATION: ch-mab6b5 heavy chain.
US-10-828-782A-18

```

Query Match	100.0%	Score 2490;	DB 5;	Length 462;
Best Local Similarity	100.0%	Pred. No. 2.9e-166;		
Matches	462;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MECSVLMFLISGTAGVLSLSEVQLQSGPELVKPGASVMSCKASGYGTDYIIMMKOSH	60	
DB	1	MECSVLMFLISGTAGVLSLSEVQLQSGPELVKPGASVMSCKASGYGTDYIIMMKOSH	60	
QY	61	GKSLWIGYITPNNGNGVNNKPKGKATLTVDKSSSTVMEKRLTSDSAVYCGRSTW	120	
DB	61	GKSLWIGYITPNNGNGVNNKPKGKATLTVDKSSSTVMEKRLTSDSAVYCGRSTW	120	
QY	121	DDFDWGGGTLTVSSASTKSPVPEPLAPCSRSTSESTAAAGCLVKDFFPEPVTVSNNG	180	
DB	121	DDFDWGGGTLTVSSASTKSPVPEPLAPCSRSTSESTAAAGCLVKDFFPEPVTVSNNG	180	
QY	181	ALTSQVHTFPVAVLSSGLYSIVTVSSNFGITQTYCNDVHKPSNKKVTKVERKCCV	240	
DB	181	ALTSQVHTFPVAVLSSGLYSIVTVSSNFGITQTYCNDVHKPSNKKVTKVERKCCV	240	
QY	241	ECPPPPAPVAGSPVFLPPPKKOTLMSRPPEVTCVVVDVSHEDPEVFQFMNVYGVGVH	300	
DB	241	ECPPPPAPVAGSPVFLPPPKKOTLMSRPPEVTCVVVDVSHEDPEVFQFMNVYGVGVH	300	
QY	301	NAKTPREDFQNSFTFRVSVLTVVHQMINKKYYCKVSNKGLPAPIEKTSKTKGQPRE	360	
DB	301	NAKTPREDFQNSFTFRVSVLTVVHQMINKKYYCKVSNKGLPAPIEKTSKTKGQPRE	360	

Db 301 NAKTYPREBQFNSTRVSVLTVVHODMLNGKEYCKYCNKGLPAPIEKTISKTKGQPRE 360
Qy 361 PQQVTLPPSRREBMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 420
Db 361 PQQVTLPPSRREBMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 420
Qy 421 LYSKLTVDKSRWQOQGNVFSQSVMEHALHNHYTQKSLISLSPGK 462
Db 421 LYSKLTVDKSRWQOQGNVFSQSVMEHALHNHYTQKSLISLSPGK 462

RESULT 2
US-09-249-011A-24
Sequence 24, Application US/09249011A
Patent No. US20020176855A1
GENERAL INFORMATION:
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARBENO, BEATRIZ
APPLICANT: CELINKER, ABIE CHERYL
APPLICANT: COLLINS, MARY
APPLICANT: GOLDMAN, SAMUEL
APPLICANT: GRAY, GARY S.
APPLICANT: KNIGHT, ANDREA
APPLICANT: O'HARA, DENISE
APPLICANT: RUP, BONITA
APPLICANT: VELDMAN, GERTREUDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
FILE REFERENCE: 08702.0081-00000
CURRENT APPLICATION NUMBER: US/09/249,011A
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 24
LENGTH: 461
TYPE: PRT
ORGANISM: Mus sp.
US-09-249-011A-24

Query Match 87.8%; Score 2185.5; DB 3; Length 461;
Best Local Similarity 88.5%; Pred. No. 6,6e-145;
Matches 409; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MECSQVMLFLSGLTAVLSRVOLOQSGPELVKPGASVQMSCKASGYGTGYIHHMKQSH 60
Db 1 MEMNCLIFLVTATGVSQVQVLQVSGAVKKPGSSVKKVSCASGYTTFDAICQVRQAP 60
Qy 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDNAVYYCGRSTW 120
Db 61 GQGLEMIQVINITIYDNTNTNOKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARAAAM 120
Qy 121 DDFDVMGQGTTLTVSASATKGPSVPLAPCSRSTSESTALGCIQVNDYPREPVTSMSNG 180
Db 121 -YMDVMGQGTTLTVSASATKGPSVPLAPCSRSTSESTALGCIQVNDYPREPVTSMSNG 179
Qy 181 ALTSQVHTPEAVLQSSGLYSLSVTVPSNSFGTQTYTCNVDHKPSNTKYDKTVERKCCV 240
Db 180 ALTSQVHTPEAVLQSSGLYSLSVTVPSNSFGTQTYTCNVDHKPSNTKYDKTVERKCCV 239
Qy 241 ECPDPCAPPAVAGPSVFLFPPKPKDITMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVA 300
Db 240 ECPDPCAPPAVAGPSVFLFPPKPKDITMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVA 299
Qy 301 NAKTYPREBQFNSTRVSVLTVVHODMLNGKEYCKYCNKGLPAPIEKTISKTKGQPRE 360
Db 301 NAKTYPREBQFNSTRVSVLTVVHODMLNGKEYCKYCNKGLPAPIEKTISKTKGQPRE 359
Qy 361 PQQVTLPPSRREBMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 420
Db 360 PQQVTLPPSRREBMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 419
Qy 421 LYSKLTVDKSRWQOQGNVFSQSVMEHALHNHYTQKSLISLSPGK 462

Db 420 LYSKLTVDKSRWQOQGNVFSQSVMEHALHNHYTQKSLISLSPGK 461

RESULT 3
US-09-859-053-28
Sequence 28, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-28

Query Match 87.3%; Score 2174; DB 3; Length 470;
Best Local Similarity 86.4%; Pred. No. 4,3e-144;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

Qy 1 MECSQVMLFLSGLTAVLSRVOLOQSGPELVKPGASVQMSCKASGYGTGYIHHMKQSH 60
Db 1 MDWTRILFLVAATGAHSQVQVLQVSGAVKKPGASVQMSCKASGYTTFGYIMHVRQAP 60
Qy 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDNAVYYCGRSTW 120
Db 61 GQGLEWMIQVINITIYDNTNTNOKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARAAAM 120
Qy 121 -----DDFDVMGQGTTLTVSASATKGPSVPLAPCSRSTSESTALGCIQVNDYPREPV 172
Db 121 YDSGQVYDADPIDWQGTMTVTVSSATKGPSVPLAPCSRSTSESTALGCIQVNDYPREPV 180
Qy 173 VTVSNNSGALTSGVHTPEAVLQSSGLYSLSVTVPSNSFGTQTYTCNVDHKPSNTKYDK 232
Db 173 VTVSNNSGALTSGVHTPEAVLQSSGLYSLSVTVPSNSFGTQTYTCNVDHKPSNTKYDK 240
Qy 233 TVERKCCVECPDPCAPPAVAGPSVFLFPPKPKDITMISRTPEVTCVVVDVSHEDPEVFQFNM 292
Db 241 TVERKCCVECPDPCAPPAVAGPSVFLFPPKPKDITMISRTPEVTCVVVDVSHEDPEVFQFNM 300
Qy 293 YVDGVEVNAKTKPREBQFNSTRVSVLTVVHODMLNGKEYCKYCNKGLPAPIEKTIS 352
Db 301 YVDGVEVNAKTKPREBQFNSTRVSVLTVVHODMLNGKEYCKYCNKGLPAPIEKTIS 360
Qy 353 KTKGQPREPQQVTLPPSRREBMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPM 412
Db 361 KTKGQPREPQQVTLPPSRREBMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPM 420
Qy 413 LQSDSFFLYSKLTVDKSRWQOQGNVFSQSVMEHALHNHYTQKSLISLSPGK 462
Db 421 LQSDSFFLYSKLTVDKSRWQOQGNVFSQSVMEHALHNHYTQKSLISLSPGK 470

RESULT 4
US-10-800-250-28
Sequence 28, Application US/10800250
Patent No. US2004014691A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Takashi

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APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, Nobuaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALIIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/10/800,250
CURRENT FILING DATE: 2004-03-10
PRIOR APPLICATION NUMBER: US/09/859,053
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-800-250-28

Query Match      87.3%; Score 2174; DB 4; Length 470;
Best Local Similarity 86.4%; Pred. No. 4.3e-144;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

QY 1 MECSVLMFLISGTAGVLSVLOOQSGPELVKPGASVVMSCKASGYTGTDYYIHMKQSH 60
DB 1 MDWTMRILFLVAATGAHSQVQLVQSGAEVKKPGASVKSVCASGYTFTGYMHWRQAP 60
QY 61 GKSLIEWIGYIYPNNGNGYNGKFKGKATLTVDKSSSTAYMELRTLTSDSAVYYGCRSTM 120
DB 61 GQGLEMMGWIMPHSGGTNYAKQFGRYMTMDTISTAYMELSRLRSDTAIVYICARTYY 120
QY 121 -----DDPDYWGQGTTLTVSSASTKGPSVFLPAPCSRSTSESTALAGCLVKDYFPEP 172
DB 121 YDSGGYHADPDWQGTMTVSSASTKGPSVFLPAPCSRSTSESTALAGCLVKDYFPEP 180
QY 173 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVPSNFGQTQYTCNVDRKPSNTXDK 232
DB 181 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVPSNFGQTQYTCNVDRKPSNTXDK 240
QY 233 TVERRKCCVCEPCPCAPPVAGPSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVQFNW 292
DB 241 TVERRKCCVCEPCPCAPPVAGPSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVQFNW 300
QY 293 YVDGEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTIS 352
DB 301 YVDGEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTIS 360
QY 353 KTKGQPREPOVYITLPPSRHEMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPM 412
DB 361 KTKGQPREPOVYITLPPSRHEMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPM 420
QY 413 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
DB 421 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 5
US-10-625-105-28
Sequence 28, Application US/10625105
GENERAL INFORMATION:
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, Nobuaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALIIM AND
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/10/625,105
CURRENT FILING DATE: 2003-07-22
```

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PRIOR APPLICATION NUMBER: US/09/859,053
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-625-105-28

Query Match      87.3%; Score 2174; DB 4; Length 470;
Best Local Similarity 86.4%; Pred. No. 4.3e-144;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

QY 1 MECSVLMFLISGTAGVLSVLOOQSGPELVKPGASVVMSCKASGYTGTDYYIHMKQSH 60
DB 1 MDWTMRILFLVAATGAHSQVQLVQSGAEVKKPGASVKSVCASGYTFTGYMHWRQAP 60
QY 61 GKSLIEWIGYIYPNNGNGYNGKFKGKATLTVDKSSSTAYMELRTLTSDSAVYYGCRSTM 120
DB 61 GQGLEMMGWIMPHSGGTNYAKQFGRYMTMDTISTAYMELSRLRSDTAIVYICARTYY 120
QY 121 -----DDPDYWGQGTTLTVSSASTKGPSVFLPAPCSRSTSESTALAGCLVKDYFPEP 172
DB 121 YDSGGYHADPDWQGTMTVSSASTKGPSVFLPAPCSRSTSESTALAGCLVKDYFPEP 180
QY 173 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVPSNFGQTQYTCNVDRKPSNTXDK 232
DB 181 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVPSNFGQTQYTCNVDRKPSNTXDK 240
QY 233 TVERRKCCVCEPCPCAPPVAGPSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVQFNW 292
DB 241 TVERRKCCVCEPCPCAPPVAGPSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVQFNW 300
QY 293 YVDGEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTIS 352
DB 301 YVDGEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTIS 360
QY 353 KTKGQPREPOVYITLPPSRHEMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPM 412
DB 361 KTKGQPREPOVYITLPPSRHEMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPM 420
QY 413 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
DB 421 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 6
US-10-292-088-46
Sequence 46, Application US/10292088
GENERAL INFORMATION:
APPLICANT: BEDIAN, YARE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PR/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 471
TYPE: PRT
ORGANISM: Homo sapiens
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SEQUENCE DESCRIPTION: SEQ ID NO: 23;
US-10-835-641-23

Query Match 86.2%; Score 2146.5; DB 5; Length 469;
Best Local Similarity 84.9%; Pred. No. 3.6e-142;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

QY 1 MECSVMFLSLGAGVLEVOLOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSH 60
DB 1 MGNSTILFLVAVANGVSEVOLVESGGGLVQPGSLALSCATSGTSTYTTTMMHMRQAP 60
QY 61 GKSLEWIGYIYPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDNAVYVYCGRSTW 120
DB 61 GKGLEWVAGINPKNGKGTSHNORFMDRFTISYDKSTAYMGNLSLRADTAAYYCAR--W 118
QY 121 DD-----FDWGOQTTLTVSSASTKSPSVFLAPCSRSTSESTALGCLVNDYDPE 171
DB 119 RGLNYPDVRYFDWGOQTTLTVSSASTKSPSVFLAPCSRSTSESTALGCLVNDYDPE 178
QY 172 PVTSMNSGALTSVHTFPVAVLOSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 231
DB 179 PVTSMNSGALTSVHTFPVAVLOSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 238
QY 232 KTVERRCCVCEPCPAPVAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVOFN 291
DB 239 KTVERRCCVCEPCPAPVAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVOFN 298
QY 292 WYVDCVFNHNAKTKREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI 351
DB 299 WYVDCVFNHNAKTKREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI 358
QY 352 SKTKQPREPOVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 411
DB 359 SKTKQPREPOVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 418
QY 412 MLDSDGSFFLYSKLTVDKSRWQGNVFSQVMEBALNHNTOKSLSLSPGK 462
DB 419 MLDSDGSFFLYSKLTVDKSRWQGNVFSQVMEBALNHNTOKSLSLSPGK 469

RESULT 9

US-10-910-901-2
; Sequence 2, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PP5
; CURRENT APPLICATION NUMBER: US/10/910,901
; PRIOR FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: Glu or Lys
; NAME/KEY: MOD RES
; LOCATION: (42)
; OTHER INFORMATION: Ser or Thr
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (97)
; OTHER INFORMATION: Ala or Pro
US-10-910-901-2

Query Match 86.2%; Score 2146; DB 5; Length 462;

Best Local Similarity 86.8%; Pred. No. 3.9e-142;
Matches 401; Conservative 23; Mismatches 38; Indels 0; Gaps 0;

QY 1 MECSVMFLSLGAGVLEVOLOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSH 60
DB 1 MDWMTSLIFLVAATGASVQVAVGAEVKKPGASVMSCKASGYTSTGFSVWRQAP 60
QY 61 GKSLEWIGYIYPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDNAVYVYCGRSTW 120
DB 61 GKGLEWVAGINPKNGKGTSHNORFMDRFTISYDKSTAYMGNLSLRADTAAYYCARYYA 120
QY 121 DDFWGOQTTLTVSSASTKSPSVFLAPCSRSTSESTALGCLVNDYDPEPPTVSNNG 180
DB 121 DYADWGOQTTLTVSSASTKSPSVFLAPCSRSTSESTALGCLVNDYDPEPPTVSNNG 180
QY 181 ALTSGVHTFPVAVLOSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYDTERKCCV 240
DB 181 ALTSGVHTFPVAVLOSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYDTERKCCV 240
QY 241 ECPPCPAPVAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVOFNMYDGEVH 300
DB 241 ECPPCPAPVAGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVOFNMYDGEVH 300
QY 301 NAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI SKTKQPRE 360
DB 301 NAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI SKTKQPRE 360
QY 361 POVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPMLSDGSFF 420
DB 421 LYSKLTVDKSRWQGNVFSQVMEBALNHNTOKSLSLSPGK 462
QY 421 LYSKLTVDKSRWQGNVFSQVMEBALNHNTOKSLSLSPGK 462

RESULT 10

US-10-822-300-138
; Sequence 138, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882, 0039, CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-138

Query Match 86.2%; Score 2145.5; DB 5; Length 446;
Best Local Similarity 89.7%; Pred. No. 4e-142;
Matches 400; Conservative 17; Mismatches 26; Indels 3; Gaps 1;

QY 20 EVOLOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSHGKSLEWIGYIYPNNGNGY 79
DB 1 QVOLVGSAGVYKKGASVYKSCASGYTFTYTMHWRQAGGQLEWNGYINPISGTYH 60
QY 80 NQKFKRATLTVDKSSSTAYMELRTLTSEDNAVYVYCGRSTWDDPD--YWGQGTTLTVSS 136
DB 61 NQKFKRATLTVDKSSSTAYMELRTLTSEDNAVYVYCGRSTWDDPD--YWGQGTTLTVSS 120
QY 137 ASTKGSVPFLAPCSRSTSESTALGCLVNDYDPEPPTVSNNSGALTSVHTFPVAVLOS 196
DB 121 ASTKGSVPFLAPCSRSTSESTALGCLVNDYDPEPPTVSNNSGALTSVHTFPVAVLOS 180
QY 197 GLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYDTERKCCVCEPCPAPVAGPSVFL 256

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Db      181 GLYSLSVYTVVSSNFGTQTTTCNDHKPSNTKVDKTVBRKCCVCEPCPCPAPAAASVF 240
Qy      257 LPPPKDQTLMSRTPEVTCVVVDVSHEDPEVQFMVYDVGVENAKTKPREEQFNSTER 316
Db      241 LPPPKDQTLMSRTPEVTCVVVDVSHEDPEVQFMVYDVGVENAKTKPREEQFNSTER 300
Qy      317 VVSVLTVVHQDMLNKEKYCKVSNKGLPAPIEKTSKTKGQPREPQVYTLPPSRREMTKN 376
Db      301 VVSVLTVVHQDMLNKEKYCKVSNKGLPAPIEKTSKTKGQPREPQVYTLPPSRREMTKN 360
Qy      377 QVSLCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSFFLYSKLTVDKSRMQQGN 436
Db      361 QVSLCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSFFLYSKLTVDKSRMQQGN 420
Qy      437 VPSCSVMHIALHNHYTQKSLSLSPGK 462
Db      421 VPSCSVMHIALHNHYTQKSLSLSPGK 446

RESULT 11
US-10-822-300-126
; Sequence 126, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; PRIORITY FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-126

Query Match      86.1%; Score 2143.5; DB 5; Length 442;
Best Local Similarity 90.1%; Pred. No. 5.5e-142;
Matches 399; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

Qy      20 EYVLOOQSGPELVKPGASVMSCKASGYTGTDTYIHHMKOSHGLSEMIQYIPNNGNGY 79
Db      1 QVQLVQSGAEVKKPKSSVSVCKASGYTFTSYRMHVRQAPQGLQEMIGYINPSTGYEY 60
Qy      80 NQKFKGKATLVDSSTAYMELRTLTSEDSAVYTCGRSTWDDPDYMGQGITLVSSAST 139
Db      61 NQKFKDQATITADSESTINAIYMEISLSRSDIAVYTCARG-GGVFDYMGQGITLVSSAST 119
Qy      140 KQPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 199
Db      120 KQPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 179
Qy      200 SISSVYTVVSSNFGTQTTTCNDHKPSNTKVDKTVBRKCCVCEPCPCPAPAAASVF 259
Db      180 SISSVYTVVSSNFGTQTTTCNDHKPSNTKVDKTVBRKCCVCEPCPCPAPAAASVF 239
Qy      260 PPKDQTLMSRTPEVTCVVVDVSHEDPEVQFMVYDVGVENAKTKPREEQFNSTER 319
Db      240 PPKDQTLMSRTPEVTCVVVDVSHEDPEVQFMVYDVGVENAKTKPREEQFNSTER 299
Qy      320 VLVVHQDMLNKEKYCKVSNKGLPAPIEKTSKTKGQPREPQVYTLPPSRREMTKNQVS 379
Db      300 VLVVHQDMLNKEKYCKVSNKGLPAPIEKTSKTKGQPREPQVYTLPPSRREMTKNQVS 359
Qy      380 LTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSFFLYSKLTVDKSRMQQGNVFS 439
Db      360 LTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSFFLYSKLTVDKSRMQQGNVFS 419
Qy      440 CSVMHIALHNHYTQKSLSLSPGK 462
Db      420 CSVMHIALHNHYTQKSLSLSPGK 442
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RESULT 12
US-11-031-485-34
; Sequence 34, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMAN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCH, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCM
; FILE REFERENCE: ABX-PP6
; CURRENT APPLICATION NUMBER: US/11/031,485
; PRIORITY FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 34
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-34

Query Match      86.1%; Score 2143.5; DB 6; Length 469;
Best Local Similarity 85.9%; Pred. No. 5.9e-142;
Matches 403; Conservative 27; Mismatches 32; Indels 7; Gaps 2;

Qy      1 MECSVMFLFLSGTNGVLSVVOLOOQSGPELVKPGASVMSCKASGYTGTDTYIHHMKOSH 60
Db      1 MDWTMSILFLVAALAGASVOLVQSGAEVKKPKGASVSVCKASGYTFTSYGINVVRQAP 60
Qy      61 GKSLEMIQYIPNNGNGVGNOKFKGKATLVDSSTAYMELRTLTSEDSAVYTC--GR 117
Db      61 GQGLKMMGMHISYISNTYTAQVQGRVTMTADTISTYMDRLSLRSDITAVYTCARGES 120
Qy      118 STWDDP---DYMGQGITLVSSASTKQPSVFPPLAPCSRSTSESTALGCLVKDYFPEPV 173
Db      121 SSSGDIYYGMDVWGQGITLVTVSSASTKQPSVFPPLAPCSRSTSESTALGCLVKDYFPEPV 180
Qy      174 TVSNMGSALTSGVHTFPAVLQSSGLYSLSSVYTVVSSNFGTQTTTCNDHKPSNTKVDKT 233
Db      181 TVSNMGSALTSGVHTFPAVLQSSGLYSLSSVYTVVSSNFGTQTTTCNDHKPSNTKVDKT 240
Qy      224 VERKCCVCEPCPCPAPAPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVQFMVY 293
Db      241 VERKCCVCEPCPCPAPAPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVQFMVY 300
Qy      294 VDGVEVHNAKTKPREEQFNSTERVSVLVTVVHQDMLNKEKYCKVSNKGLPAPIEKTSK 353
Db      301 VDGVEVHNAKTKPREEQFNSTERVSVLVTVVHQDMLNKEKYCKVSNKGLPAPIEKTSK 360
Qy      354 TKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPML 413
Db      361 TKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPML 420
Qy      414 DSDGSFFLYSKLTVDKSRMQQGNVFSQVMHIALHNHYTQKSLSLSPGK 462
Db      421 DSDGSFFLYSKLTVDKSRMQQGNVFSQVMHIALHNHYTQKSLSLSPGK 469

RESULT 13
US-10-822-300-136
; Sequence 136, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
```

```

: CURRENT FILING DATE: 2004-04-09
: NUMBER OF SEQ ID NOS: 146
: SOFTWARE: Patencin version 3.2
: SEQ ID NO 136
: LENGTH: 446
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-822-300-136

```

Query Match	86.0%;	Score 2142.5;	DB 5;	Length 446;
Best Local Similarity	89.7%;	Pred. No. 6.5e-142;		
Matches 400;	Conservative 16;	Mismatches 27;	Indels 3;	Gaps 1,

Qy	20	EVOLQOOSPELVKCPASVYMSCKAGYSTDYIHHMKOSHGLSEMIQIYIYNNGANG	79
Db	1	QVQLVQSGAEVKKRPASVYVSCSKASGYTITSTTHMVRQAPRQGLEMTGINRSGYTH	60
Qy	80	NQKEKKAITLVDSKSSSTAYMELRITLTSDSAIVYTCGRSTWDF--YWGQSTLTIVSS	136
Db	61	NQKLDKKATITLVADKASSTAYTMELSSIRSEDTAVVYCARSAAYDYDPAFWGQSTLTIVSS	120
Qy	137	ASTGSPAPPLAPCGRSTSESTAAIGCVKDYFPREPVYVSNMGSALTSCTHPHRAIQSS	196
Db	121	ASTKPSVFPPLAPCGRSTSESTAAIGCVKDYFPREPVYVSNMGSALTSCTHPTPAIQSS	180
Qy	197	GLYSLSSVYVTPSSNFGIQTYYTNCNDHKSNNKVDKTVERRCKCCECPCPAPRVAQPSVF	256
Db	181	GLYSLSSVYVTPSSNFGIQTYYTNCNDHKSNNKVDKTVERRCKCCECPCPAPPAAPSVF	240
Qy	257	LPPEPKQDTLMSTRPEVTCTVVVDYSHDEPQVFNKTVDGVEYHNAKTYKPREQFNSTER	316
Db	241	LPPEPKQDTLMSTRPEVTCTVVVDYSHDEPQVFNKTVDGVEYHNAKTYKPREQFNSTER	300
Qy	317	VVSUTLVVHOMDLNKGKEYCKVSNGLPAPIEKTISKTKGQPREPOVYTLPREREEMTN	376
Db	301	VVSUTLVVHOMDLNKGKEYCKVSNGLPAPIEKTISKTKGQPREPOVYTLPREREEMTN	360
Qy	377	QVSLTCLVKGPYPSDIAVWESNCGQPENNYKTTPLMLDSGSEFLYSKLTVDSKRWQGN	436
Db	361	QVSLTCLVKGPYPSDIAVWESNCGQPENNYKTTPLMLDSGSEFLYSKLTVDSKRWQGN	420
Qy	437	VFSCSVMEHALHNHYTKSLSTSPCK 462	
Db	421	VFSCSVMEHALHNHYTKSLSTSPCK 446	

```

RESULT 14
US-10-822-300-137
; Sequence 137, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcγR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-137

```

Query Match 86.0%; Score 2142.5; DB 5; Length 446;
 Best Local Similarity 89.7%; Pred. No. 6,5e-142;
 Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1

QY 20 EVQLQQSGPELVKPSASVYMGSKASGYGTDYYIHMKQSHKSLSEMTGYLYENNNGANGY 79
 DB 1 QVQLVQSSAEVYKPPASVYVSKASGYGTFITSTHMKVDAPOGLGEMMGYINFRGGYTHY 60

[illegible]

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RESULT 15
US-10-822-300-124
; Sequence 124, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCγR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 442
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-822-300-124

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Query Match	86.0%	Score 2140.5	DB 5	Length 442
Best Local Similarity	90.1%	Pred. 8.9e-142		
Matches	399	Conservative 17	Mismatches 26	Indels 1; Gaps 1
QY	20	EVQLQDSPEPELVKSPASVYKMSCKASGYGTDVYIHMMQSHSKSLSEMIYIYPNNKGANCY	79	
Db	1	QVQLVQSAEYKRRKSSVYKSCSKASGYFTFSRTHMVAQAPQGLEIMCIYINPSTGYTEX	60	
QY	80	NQKFKGAKTLITVDKSSSTAYMELRTLTISEDSAVVYCGSRSTWDDFDYWGQGITLVSSAST	139	
Db	61	NQKFDKAKTITADESTINTAYMELSLRSBDDTAIVYICARG-GGVFDYWGQGITLVTSASAT	119	
QY	140	KGPSVFPLAPCSRSTSESTAALGCLVADYFPEPPTVSWNSGALTSGVHTFPAVLQSSGLY	199	
Db	120	KGPSVFPLAPCSRSTSESTAALGCLVADYFPEPPTVSWNSGALTSGVHTFPAVLQSSGLY	179	
QY	200	SLSSVTVVPSNFGQYTCNVADHKSNTKVDKTYERKCCVCEPCCPAPPAVAGSPVFLFP	259	
Db	180	SLSSVTVVPSNFGYTCNVADHKSNTKVDKTYERKCCVCEPCCPAPPAVAGSPVFLFP	239	
QY	260	PKPKDTLLMISRTPEYTCVVVDVSHEDPEVFQWYVDGVEVHNAKTKPRREQDSTFRVVS	319	
Db	240	PKPKDMLMISRTPEYTCVVVDVSHEDPEVFQWYVDGVEVHNAKTKPRREQDSTFRVVS	299	
QY	320	VLTVVHODMLNGEKYCKVSNKGLPAPLEKTIKTKGAPREFQVYTLPPSRDEMTKNQVS	379	

[illegible]

Db	300	VLTVVHODWLNKSKYCKVSNKGLPALEKTSKTKGQPREPOVYTLPPSRREMTKNQVS	359
Qy	380	LTCLVKGFPSPDIAVEMBSNGOPENNYKTPPMLDSDGSFFLYSKLTVDKSRMOQGNVFS	439
Db	360	LTCLVKGFPSPDIAVEMBSNGOPENNYKTPPMLDSDGSFFLYSKLTVDKSRMOQGNVFS	419
Qy	440	CSVMHEALHNHYTKXSLSPGK	462
Db	420	CSVMHEALHNHYTKXSLSPGK	442

Search completed: January 24, 2006, 19:13:08
Job time : 114.021 secs


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Db      240 VECPCPAPPAAPVFLFPPPKDTLMSRTPEYTCVVVDVSHEDPEVFQFMVYDQVEV 299
Qy      300 HNAKTPREEQFNSTFRVVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR 359
Db      300 HNAKTPREEQFNSTFRVVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR 359
Qy      360 EPOVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTPMLDSDGF 419
Db      360 EPOVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTPMLDSDGF 419
Qy      420 FLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTOKSLSLSPGK 462
Db      420 FLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTOKSLSLSPGK 462

RESULT 2
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039nak1
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match      87.3%; Score 2174; DB 2; Length 470,
Best Local Similarity 86.4%; Pred. No. 1.1e-157;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

Qy      1 MECSGMLFLSAGTGVLSVQLOQSGPELVKPGASVKNKSCASGYTGTDTYIHMKNQSH 60
Db      1 MDWTRILFLVAALTAAGASQVQVLOSAGAEVKKPGASVKNKSCASGYTGTDTYIHMKNQSH 60
Qy      61 GKSLEMIIGIYIPNNGNGNGYOKFKGKATLTVDKSSSTAYMELRTLTSBDSAVYCGRSTW 120
Db      61 GGLGLEMWGINPSSGNTVYAKQFGKRVMTTRDTLSISTAYMELSRILSDDTAVYCARVY 120
Qy      121 -----DDPYWGQGTTLTVSSASTKPSVFPPLAPCSRSTSESTAAIGCLVCKYFPEP 172
Db      121 YDSGGYTHAFPIWQGTWTVTSASTKPSVFPPLAPCSRSTSESTAAIGCLVCKYFPEP 180
Qy      173 VTVSNMNGALTSQVHTFPAYLOSGLYSLSVTVTPSSNFGTQTYTQCNVDHKPSNTKVDX 232
Db      181 VTVSNMNGALTSQVHTFPAYLOSGLYSLSVTVTPSSNFGTQTYTQCNVDHKPSNTKVDX 240
Qy      233 TVERRKCCVBCPCAPAPVAGPSVFLFPPPKDTLMSRTPEYTCVVVDVSHEDPEVQFMW 292
Db      241 TVERRKCCVBCPCAPAPVAGPSVFLFPPPKDTLMSRTPEYTCVVVDVSHEDPEVQFMW 300
Qy      293 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTIS 352
Db      301 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTIS 360
Qy      363 KTKGQPRBPOVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTPM 412
Db      361 KTKGQPRBPOVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTPM 420

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Qy      413 LDSGSEFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTOKSLSLSPGK 462
Db      421 LDSGSEFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTOKSLSLSPGK 470

RESULT 3
US-07-934-373C-23
; Sequence 23, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-23

Query Match      86.2%; Score 2146.5; DB 1; Length 469;
Best Local Similarity 84.9%; Pred. No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

Qy      1 MECSGMLFLSAGTGVLSVQLOQSGPELVKPGASVKNKSCASGYTGTDTYIHMKNQSH 60
Db      1 MGSMSIILFLVATATGAVSEVQLVBSGGGLVQPGSLRLSCATSGYTFLEYTHMKNQSH 60
Qy      61 GKSLEMIIGIYIPNNGNGNGYOKFKGKATLTVDKSSSTAYMELRTLTSBDSAVYCGRSTW 120
Db      61 GKSLEMIIGIYIPNNGNGNGYOKFKGKATLTVDKSSSTAYMELRTLTSBDSAVYCGRSTW 118
Qy      121 DD-----FDYWGQGTTLTVSSASTKPSVFPPLAPCSRSTSESTAAIGCLVNDYFPE 171
Db      119 RGATNGFVRIFDVWGQGTTLTVSSASTKPSVFPPLAPCSRSTSESTAAIGCLVNDYFPE 178
Qy      172 PTVSNMNGALTSQVHTFPAYLOSGLYSLSVTVTPSSNFGTQTYTQCNVDHKPSNTKVD 231
Db      179 PTVSNMNGALTSQVHTFPAYLOSGLYSLSVTVTPSSNFGTQTYTQCNVDHKPSNTKVD 238
Qy      232 KTVERRKCCVBCPCAPAPVAGPSVFLFPPPKDTLMSRTPEYTCVVVDVSHEDPEVQFN 291

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Db 239 KTVKRCCECPBPAPVAGPSVFLPPPKKDTLMTSRTEVATCVVDVSHEDPEVOFN 298
Qy 292 WYVDGEVHNAKTPREBOFNSTFRVSVLTIVHODMLNGKEYCKVSNKGLPAPIEKT 351
Db 299 WYDGMVHNAKTPREBOFNSTFRVSVLTIVHODMLNGKEYCKVSNKGLPAPIEKT 358
Qy 352 SKTKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPDSIDIAVWESNGOPENNYKTPP 411
Db 359 SKTKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPDSIDIAVWESNGOPENNYKTPP 418
Qy 412 MLDSGSPFLYSKLTVDKSRWQGNVSCSVMEALHNHTYOKSLSPGK 462
Db 419 MLDSGSPFLYSKLTVDKSRWQGNVSCSVMEALHNHTYOKSLSPGK 469

RESULT 4
US-08-437-642B-23
Sequence 23, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437, 642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-437-642B-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;
Best Local Similarity 84.9%; Pred No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

Qy 1 MECSCVMLPLISAGTAVLSEVQLQSGPELVKPGASVVMKSCAKSGYTGTDYIYHMKQSH 60
Db 1 MGVMSCTILFLVATAGVHSEVQLVSGGGLVPGGSLSLSCATSYTLETETMHWNRQAP 60

Qy 61 GKSLIEWIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSEDSAVVYCGHSTW 120
Db 61 GKSLIEWAGINPKKGGSHNRFPMDRTISVDKSTSTAYMQMNSLRADTAVVYCAR--W 118
Qy 121 DD-----FDYWGQGITLTSSASTKGPSPVPLAPCSHSTSESTALCLVYDYPE 171
Db 119 RGLNYGFDVRYFDWVGQGITLVTSASTKGPSPVPLAPCSHSTSESTALCLVYDYPE 178
Qy 172 PVTVMNSGALTSGVHPFPALQSSGLYSLSVTVTSNNGTTCNVDRKPSNTVD 231
Db 179 PVTVMNSGALTSGVHPFPALQSSGLYSLSVTVTSNNGTTCNVDRKPSNTVD 238
Qy 232 KTVKRCCECPBPAPVAGPSVFLPPPKKDTLMTSRTEVATCVVDVSHEDPEVOFN 291
Db 239 KTVKRCCECPBPAPVAGPSVFLPPPKKDTLMTSRTEVATCVVDVSHEDPEVOFN 298
Qy 292 WYVDGEVHNAKTPREBOFNSTFRVSVLTIVHODMLNGKEYCKVSNKGLPAPIEKT 351
Db 299 WYDGMVHNAKTPREBOFNSTFRVSVLTIVHODMLNGKEYCKVSNKGLPAPIEKT 358
Qy 352 SKTKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPDSIDIAVWESNGOPENNYKTPP 411
Db 359 SKTKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPDSIDIAVWESNGOPENNYKTPP 418
Qy 412 MLDSGSPFLYSKLTVDKSRWQGNVSCSVMEALHNHTYOKSLSPGK 462
Db 419 MLDSGSPFLYSKLTVDKSRWQGNVSCSVMEALHNHTYOKSLSPGK 469

RESULT 5
US-08-146-206C-23
Sequence 23, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146, 206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-146-206C-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;

Best Local Similarity 84.9%; Pred. No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

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QY 1 MECSGMFLISGTVAGVSEVOLQOOSGPELVKPGASVMSCKASGTYGTDYIHMKQSH 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 MMSGCIILFLVATATGVSHEVOLVESGGGLVQPGSLRLSCATSGTTFTEYTHMMRQAP 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSDSAVYYCGRSTW 120
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 61 GKGLEWVAGINPKNGGTHNORFMDRFTISVDKSTSTAYMOMNSLRABDTAVYYCAR--W 118
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 DD-----FDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSTSTAALGCLVADYFPE 171
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 119 RGLNAGFDVRYFDVWGQGTTLTVSSASTKGSVFPLAPCSRSTSTSTAALGCLVADYFPE 178
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 172 PVTVMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 231
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 179 PVTVMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 238
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 232 KTVKRCCKVCEPCPCAPPVAGPSVFLFPPKPDQTLMIKRTPEVTCVVDVSHEDPEVQFN 291
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 239 KTVKRCCKVCEPCPCAPPVAGPSVFLFPPKPDQTLMIKRTPEVTCVVDVSHEDPEVQFN 298
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 292 WYVDGMEVHNAKTKREBOFNSTFRVSVLTVVHODMNGKEYCKCKVSNKGLPADIEKTI 351
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 299 WYVDGMEVHNAKTKREBOFNSTFRVSVLTVVHODMNGKEYCKCKVSNKGLPADIEKTI 358
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 352 SKTKGQPREPOVYITLPFSREEMTKQVSLTCLVKGFPYSDIAVEESNQGPENNYKTTTP 411
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 359 SKTKGQPREPOVYITLPFSREEMTKQVSLTCLVKGFPYSDIAVEESNQGPENNYKTTTP 418
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 412 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 462
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 419 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 469
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

RESULT 6

US-09-705-686-23
Sequence 23, Application US/09705686
Patent No. 6639055

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NO. 6639055-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-705-686-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;

Best Local Similarity 84.9%; Pred. No. 1.4e-155;

Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

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QY 1 MECSGMFLISGTVAGVSEVOLQOOSGPELVKPGASVMSCKASGTYGTDYIHMKQSH 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 MMSGCIILFLVATATGVSHEVOLVESGGGLVQPGSLRLSCATSGTTFTEYTHMMRQAP 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSDSAVYYCGRSTW 120
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 61 GKGLEWVAGINPKNGGTHNORFMDRFTISVDKSTSTAYMOMNSLRABDTAVYYCAR--W 118
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 DD-----FDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSTSTAALGCLVADYFPE 171
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 119 RGLNAGFDVRYFDVWGQGTTLTVSSASTKGSVFPLAPCSRSTSTSTAALGCLVADYFPE 178
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 172 PVTVMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 231
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 179 PVTVMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 238
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 232 KTVKRCCKVCEPCPCAPPVAGPSVFLFPPKPDQTLMIKRTPEVTCVVDVSHEDPEVQFN 291
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 239 KTVKRCCKVCEPCPCAPPVAGPSVFLFPPKPDQTLMIKRTPEVTCVVDVSHEDPEVQFN 298
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 292 WYVDGMEVHNAKTKREBOFNSTFRVSVLTVVHODMNGKEYCKCKVSNKGLPADIEKTI 351
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 299 WYVDGMEVHNAKTKREBOFNSTFRVSVLTVVHODMNGKEYCKCKVSNKGLPADIEKTI 358
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 352 SKTKGQPREPOVYITLPFSREEMTKQVSLTCLVKGFPYSDIAVEESNQGPENNYKTTTP 411
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 359 SKTKGQPREPOVYITLPFSREEMTKQVSLTCLVKGFPYSDIAVEESNQGPENNYKTTTP 418
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 412 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 462
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 419 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 469
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

RESULT 7

US-09-705-392A-23

Sequence 23, Application US/09705392A
Patent No. 671971

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-NO. 671971-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-705-392A-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;
 Best Local Similarity 84.9%; Pred. No. 1.4e-155;
 Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

QY 1 MECSGVMFLSTGTVLSEVLOOQSGPELVKPGASVMSCKASGYTGTDYIHHMKOSH 60
 DB 1 MGMSCLILFLVATANGVHSEVQVLESQGLVQPGSLRLSCATSGYTFTEYTHMMRQAP 60
 QY 61 GKSLFMIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLSEDSAVYYCGRSTW 120
 DB 61 GKGLEWVAGINPKNGGTSNQRFMDFITISVDKSTSTAYMOMNSLRADTAVYYCAR--W 118
 QY 121 DD-----FDVWGQSTTLTVSSASTKGPSPVPLAPCSRSTSESTAALGCLVNDYPE 171
 DB 119 RGLNYGPDVRYFDVWGQSTLTVSSASTKGPSPVPLAPCSRSTSESTAALGCLVNDYPE 178
 QY 172 PVTVMNSGALTSQVHTTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYD 231
 DB 179 PVTVMNSGALTSQVHTTPPAVLQSSGLYSLSVTVVTSNFGTQYTCNVDHKPSNTKYD 238
 QY 232 KTVKRCCEVCPCCPAPVAGPSVFLPPPKDQTLMISTRPEVTCVVDVSHEDDEVQFN 291
 DB 239 KTVKRCCEVCPCCPAPVAGPSVFLPPPKDQTLMISTRPEVTCVVDVSHEDDEVQFN 298
 QY 292 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPADIETKI 351
 DB 299 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPADIETKI 358
 QY 352 SKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 411
 DB 359 SKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 418
 QY 412 MLDSDGSFFLYSKLTVDKSRWQQGVFSCSVHHEALHHNYTOKSLSPGK 462
 DB 419 MLDSDGSFFLYSKLTVDKSRWQQGVFSCSVHHEALHHNYTOKSLSPGK 469

RESULT 8
 US-09-705-398-23
 Sequence 23, Application US/09705398
 Patent No. 6800738

GENERAL INFORMATION:
 APPLICANT: Carter, Paul J.
 PRESENT: Presta, Leonard G.
 TITLE OF INVENTION: Method for Making Humanized Antibodies
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/705,398
 FILING DATE: 02-NOV-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-705-398-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;
 Best Local Similarity 84.9%; Pred. No. 1.4e-155;
 Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

QY 1 MECSGVMFLSTGTVLSEVLOOQSGPELVKPGASVMSCKASGYTGTDYIHHMKOSH 60
 DB 1 MGMSCLILFLVATANGVHSEVQVLESQGLVQPGSLRLSCATSGYTFTEYTHMMRQAP 60
 QY 61 GKSLFMIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLSEDSAVYYCGRSTW 120
 DB 61 GKGLEWVAGINPKNGGTSNQRFMDFITISVDKSTSTAYMOMNSLRADTAVYYCAR--W 118
 QY 121 DD-----FDVWGQSTTLTVSSASTKGPSPVPLAPCSRSTSESTAALGCLVNDYPE 171
 DB 119 RGLNYGPDVRYFDVWGQSTLTVSSASTKGPSPVPLAPCSRSTSESTAALGCLVNDYPE 178
 QY 172 PVTVMNSGALTSQVHTTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYD 231
 DB 179 PVTVMNSGALTSQVHTTPPAVLQSSGLYSLSVTVVTSNFGTQYTCNVDHKPSNTKYD 238
 QY 232 KTVKRCCEVCPCCPAPVAGPSVFLPPPKDQTLMISTRPEVTCVVDVSHEDDEVQFN 291
 DB 239 KTVKRCCEVCPCCPAPVAGPSVFLPPPKDQTLMISTRPEVTCVVDVSHEDDEVQFN 298
 QY 292 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPADIETKI 351
 DB 299 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPADIETKI 358
 QY 352 SKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 411
 DB 359 SKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 418
 QY 412 MLDSDGSFFLYSKLTVDKSRWQQGVFSCSVHHEALHHNYTOKSLSPGK 462
 DB 419 MLDSDGSFFLYSKLTVDKSRWQQGVFSCSVHHEALHHNYTOKSLSPGK 469

RESULT 9
 US-09-301-593-30
 Sequence 30, Application US/09301593A
 Patent No. 6455677

GENERAL INFORMATION:
 APPLICANT: Park, John E.
 APPLICANT: Garin-Chesa, Pilar
 APPLICANT: Bamberger, Uwe
 APPLICANT: Leger, Olivier
 APPLICANT: Saldanha, Jose W.

```

/ APPLICANT: Rettig, Wolfgang J
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ CURRENT FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 30
/ LENGTH: 472
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-30

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Query Match      85.5%; Score 2128; DB 2; Length 472;
Best Local Similarity 86.7%; Pred. No. 3,7e-154;
Matches 410; Conservative 20; Mismatches 31; Indels 12; Gaps 5;

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QY 1 MECSQVMEFLSLGTAAGVSEVQLQDSGPRLVRPGAQSVKSKCKASGYGTDYYIHMMKQSH 60
DB 1 MMSWVFLFLSLGTAAGVSEVQLQDSGPRLVRPGAQSVKSKCKASGYGTDYYIHMMKQSH 60
QY 61 GKSLEWIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSEDNAVYYCGRST- 119
DB 61 GKSLEWIGIIPNNGIIPNNOKEKGRATLTVGKSSSTAYMELRTLTSEDNAVYYFCARRI 120
QY 120 ---WMD---FDVWGQTTLTSSASATKGSVPPLAPCSSTSESTALGCLVQDYPRPV 173
DB 121 AVYGEHGMADWQGTSTVSS-STKGSVPPLAPSSKSTSGTALGCLVQDYPRPV 179
QY 174 TVSMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCNVDHKPSNTKVDRT 233
DB 180 TVSMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCNVDHKPSNTKVDK 239
QY 234 VERKCCVE---CPKCPAP-VAQPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQ 289
DB 240 VERKCCDKHTCPKCPAPFLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVK 299
QY 290 FMYVYDGVVHNAKTRREQNRSTPRVYSLTVVHODPLNGKRYCKVSNGLPAPIEK 349
DB 300 FMYVYDGVVHNAKTRREQNRSTPRVYSLTVVHODPLNGKRYCKVSNGLPAPIEK 359
QY 350 TISKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKT 409
DB 360 TISKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKT 419
QY 410 PMLDSDGSFFLYSKLTVDKSRWQQGVFSCSYVMEHALAHNYTKSLSPGK 462
DB 420 PVLDSGDSFFLYSKLTVDKSRWQQGVFSCSYVMEHALAHNYTKSLSPGK 472

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RESULT 10
PCT-US93-07832-23

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/ Sequence 23, Application PC/TUS9307832
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patin (Genentech)

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07832
/ FILING DATE: 19930820
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/715272
/ FILING DATE: 14-JUN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05126
/ FILING DATE: 15-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/934373
/ FILING DATE: 21-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME:
/ REGISTRATION NUMBER:
/ REFERENCE/DOCKET NUMBER: 709P2PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE:
/ TELEFAX: 415/952-9881
/ TELEEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 552 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
PCT-US93-07832-23

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Query Match      84.8%; Score 2111.5; DB 4; Length 552;
Best Local Similarity 76.8%; Pred. No. 8.2e-153;
Matches 400; Conservative 27; Mismatches 33; Indels 61; Gaps 3;

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QY 1 MECSQVMEFLSLGTAAGVSEVQLQDSGPRLVRPGAQSVKSKCKASGYGTDYYIHMMKQSH 60
DB 34 MMSWVFLFLSLGTAAGVSEVQLQDSGPRLVRPGAQSVKSKCKASGYGTDYYIHMMKQSH 93
QY 61 GKSLEWIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSEDNAVYYCGRSTW 120
DB 94 GKSLEWVAGINPKNGKGTSHNORFMDRTISVDKSTSIYMOGNSLRADTAAYTCAR--W 151
QY 121 DD-----FDVWGQTTLTSSASATKGSVPPLAPCSSTSESTALGCLVQDYPRPV 171
DB 152 RGLNATGFDVRYFDVWGQTLTVSSASATKGSVPPLAPCSSTSESTALGCLVQDYPR 211
QY 172 TVSMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCNVDHKPSNTKVD 231
DB 212 PVTVMNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCNVDHKPSNTKVD 271
QY 232 KTVERRCCV-----E 241
DB 272 KTVERRCCVTCPPCPAPFLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVK 331
QY 242 CPPCPAPVAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQPMVVDGVEVHN 301
DB 332 CPPCPAPVAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQPMVVDGVEVHN 391
QY 302 AKTKPREQNFSTPRVYSLTVVHODPLNGKRYCKVSNGLPAPIEKTISTKQPREP 361
DB 392 AKTKPREQNFSTPRVYSLTVVHODPLNGKRYCKVSNGLPAPIEKTISTKQPREP 451
QY 362 QVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPMLDSDGSFFL 421
DB 452 QVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPMLDSDGSFFL 511
QY 422 YSKLTVDKSRWQQGVFSCSYVMEHALAHNYTKSLSPGK 462
DB 512 YSKLTVDKSRWQQGVFSCSYVMEHALAHNYTKSLSPGK 552

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RESULT 11
US-08-788-800-12

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/ Sequence 12, Application US/08788800
/ Patent No. 5914112

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GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-12

Query Match      84.5%; Score 2103.5; DB 1; Length 450;
Best Local Similarity 86.5%; Pred. No. 2,6e-152;
Matches 391; Conservative 23; Mismatches 27; Indels 11; Gaps 2;

QY 20 EVLOQSGPELVKPGASVMSCKASGYGTDYIYHMKQSHKSLSEWIGYIPNNNGXGY 79
DB 1 EVLVESGGGLVQPGSLRLSCATSGYTFEYTHMMQAPKGLFWAGINPKKGGTSH 60
QY 80 NQKFKGKATLVVDKSSSTAYNELRTLTSBDSAVYTCGSTWMD-----FDYWGQGT 130
DB 61 NQKFKGKATLVVDKSSSTAYNELRTLTSBDSAVYTCGSTWMD-----FDYWGQGT 118
QY 131 TLTVSSASTKGPSPVPLAPCSRSTSESTALGCLVKDYFPEPVTVYSNMSGALTSGVHPP 190
DB 119 LVTSSASTKGPSPVPLAPCSRSTSESTALGCLVKDYFPEPVTVYSNMSGALTSGVHPP 178
QY 191 AVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVKCCVCECPPCAPPV 250
DB 179 AVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVKCCVCECPPCAPPV 238
QY 251 AGPSVFLPPPKKDTLMI SRTEPEVTCVVVDVSHEDPEVQFMNYYVDGVEVHNAKTPRBEQ 310
DB 239 AGPSVFLPPPKKDTLMI SRTEPEVTCVVVDVSHEDPEVQFMNYYVDGVEVHNAKTPRBEQ 298
QY 311 FNSTRRVSVTLTVHQMQLNGKCYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR 370
DB 299 FNSTRRVSVTLTVHQMQLNGKCYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR 358
QY 371 EEMTKNQVSLTCLVGFPSPDIAVEMESNQGPENNYKTPPMLDSDGSFPLYSKLTVDKS 430
DB 359 EEMTKNQVSLTCLVGFPSPDIAVEMESNQGPENNYKTPPMLDSDGSFPLYSKLTVDKS 418
QY 431 RMQOGNVSFCSVHMEALHNHYTQKSLSLSPGK 462
DB 419 RMQOGNVSFCSVHMEALHNHYTQKSLSLSPGK 450

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RESULT 12
US-09-238-741-4
Sequence 4, Application US/09238741
Patent No. 6897044
GENERAL INFORMATION:
APPLICANT: BRASLAWSKY, GARY R.
APPLICANT: HANNA, NABIL
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: LABAREE, MICHAEL J.
APPLICANT: HUTNH, TRI B.
TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
FILE REFERENCE: 23522,0584
CURRENT APPLICATION NUMBER: US/09/238,741
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match      83.7%; Score 2084; DB 2; Length 470;
Best Local Similarity 84.0%; Pred. No. 8.3e-151;
Matches 395; Conservative 27; Mismatches 40; Indels 8; Gaps 3;

QY 1 MECSVMLFLSLGAGVLSVQLQSGPELVKPGASVMSCKASGYGTDYIYHMKQSH 60
DB 1 MGSLLILFLVAVAATRVLSVQLQSGPELVKPGASVMSCKASGYGTDYIYHMKQSH 60
QY 61 GKSLEWIGYIPNNNGNGYNQKFKGKATLVVDKSSSTAYNELRTLTSBDSAVYTCGSTW 120
DB 61 GRGLEWIGYIPNGNDTSYNOKFKGKATLVVDKSSSTAYNELRTLTSBDSAVYTCGSTW 120
QY 121 DD---FDYWGQGTTLTVSSASTKGPSPVPLAPCSRSTSESTALGCLVKDYFPEPVTVS 176
DB 121 YGDGMYFVNWAGCTVTVSSASTKGPSPVPLAPCSRSTSESTALGCLVKDYFPEPVTVS 180
QY 177 MNSGLTSGVTHFPVAVLDSSGLYSLSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVK 236
DB 181 MNSGLTSGVTHFPVAVLDSSGLYSLSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVK 240
QY 237 KCVE---CPKCPAPP-VAGPSVFLPPPKKDTLMI SRTEPEVTCVVVDVSHEDPEVQFMN 292
DB 241 KSCDKHTKCPKCPAPP-VAGPSVFLPPPKKDTLMI SRTEPEVTCVVVDVSHEDPEVQFMN 300
QY 293 YVDGVEVHNAKTKRBEQFNSTFRVSVTLTVHQMQLNGKCYKCKVSNKGLPAPIEKTIS 352
DB 301 YVDGVEVHNAKTKRBEQFNSTFRVSVTLTVHQMQLNGKCYKCKVSNKGLPAPIEKTIS 360
QY 353 KTKGQPREPQVYTLPPSRSEEMTKNQVSLTCLVGFPSPDIAVEMESNQGPENNYKTPPM 412
DB 361 KAKGQPREPQVYTLPPSRSEEMTKNQVSLTCLVGFPSPDIAVEMESNQGPENNYKTPPM 420
QY 413 LQSDGSFPLYSKLTVDKSRMGOQNVFSCVHMEALHNHYTQKSLSLSPGK 462
DB 421 LQSDGSFPLYSKLTVDKSRMGOQNVFSCVHMEALHNHYTQKSLSLSPGK 470

RESULT 13
US-09-472-087-2
Sequence 2, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, BILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.

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QY 21 VOLQOSGBELVKGASVVMSCASGYTGTDYIHHMKOSHGSLEWIGIYYNNNGNGYN 80
Db 1 VOLQOSGBELVKGASVVMSCASGYTGTDYIHHMKOSHGSLEWIGIYYNNNGNGYN 60
QY 81 QKFKGKATLTVDKSSSTAAMELRLTJSEDSAVYYCGRST---WMD---PDYWGQTTLT 133
Db 61 QKFKGKATLTVDKSSSTAAMELRLTJSEDSAVYFCARRRIAYGYDEGHAMDYWGQTSVT 120
QY 134 VSSASTKGPSPVPLAPCSRSTSESTALGCLVKQYFPEPPTVSWNSGALTSGVHTFPAVL 193
Db 121 VSSASTKGPSPVPLAPSSKSTSGGTALGCLVKQYFPEPPTVSWNSGALTSGVHTFPAVL 180
QY 194 QSSGLYSLSVYTPSSNFGTQTYTCNVDHKPSNTKVDKVERKCCVE---CPPCPAPP- 249
Db 181 QSSGLYSLSVYTPSSSLGTQTYTCNVNHPKSNTKVDKVEPKSCDKHTHCPCPAPEL 240
QY 250 VAGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVQFNMYVDGYEVHNAKTKPREE 309
Db 241 LGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGYEVHNAKTKPREE 300
QY 310 QFNSTFRVSVLTIVHQMINKKEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPS 369
Db 301 QYNSTFRVSVLTIVHQMINKKEYCKVSNKGLPAPIEKTISKAKQPREPQVYTLPPS 360
QY 370 REEMTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNKTTPMLDSDGSPFLYSKLTVDK 429
Db 361 REEMTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNKTTPPVLDSGSPFLYSKLTVDK 420
QY 430 SRMOQGNVFCSCVMHEALHNHYTKSLSPGK 462
Db 421 SRMOQGNVFCSCVMHEALHNHYTKSLSPGK 453
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Search completed: January 24, 2006, 18:58:34
Job time : 43.6395 secs

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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